pD17-cJ-dCH2.H1

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        10          20          30          40          50          60          70          80          90
GACGGATCGG  GAGATCTGCT  AGGTGACCTG  AGGGCGCCCG  GCTTCGAATA  GCCAGAGTAA  CCTTTTTTTT  TAATTTTATT  TTATTTTATT
CTGCCTAGCC  CTCTAGACGA  TCCACTGGAC  TCCCGCGCGC  CGAAGCTTAT  CGGTCTCATT  GGAAAAAAAA  ATTAAAAATAA AATAAAATAA

       100         110         120         130         140         150         160         170         180
TTTGAGATGG  AGTTTGGCGC  CGATCTCCCG  ATCCCCTATG  GTCGACTCTC  AGTACAATCT  GCTCTGATGC  CGCATAGTTA  AGCCAGTATC
AAACTCTACC  TCAAACGCCG  GCTAGAGGGC  TAGGGGATAC  CAGCTGAGAG  TCATGTTAGA  CGAGACTACG  GCGTATCAAT  TCGGTCATAG

       190         200         210         220         230         240         250         260         270
TGCTCCCTGC  TTGTGTGTTG  GAGGTCGCTG  AGTAGTGCGC  GAGCAAAATT  TAAGCTACAA  CAAGGCAAGG  CTTGACCGAC  AATTGCATGA
ACGAGGGACG  AACACACAAC  CTCCAGCGAC  TCATCACGCG  CTCGTTTTAA  ATTCGATGTT  GTTCCGTTCC  GAACTGGCTG  TTAACGTACT

       280         290         300         310         320         330         340         350         360
AGAATCTGCT  TAGGGTTAGG  CGTTTTGCGC  TGCTTCGCGA  TGTACGGGCC  AGATATACGC  GTTGACATTG  ATTATTGACT  AGTTATTAAT
TCTTAGACGA  ATCCCAATCC  GCAAAACGCG  ACGAAGCGCT  ACATGCCCGG  TCTATATGCG  CAACTGTAAC  TAATAACTGA  TCAATAATTA

       370         380         390         400         410         420         430         440         450
AGTAATCAAT  TACGGGGTCA  TTAGTTCATA  GCCCATATAT  GGAGTTCCGC  GTTACATAAC  TTACGGTAAA  TGGCCCGCCT  GGCTGACCGC
TCATTAGTTA  ATGCCCCAGT  AATCAAGTAT  CGGGTATATA  CCTCAAGGCG  CAATGTATTG  AATGCCATTT  ACCGGGCGGA  CCGACTGGCG

       460         470         480         490         500         510         520         530         540
CCAACGACCC  CCGCCCATTG  ACGTCAATAA  TGACGTATGT  TCCCATAGTA  ACGCCAATAG  GGACTTTCCA  TTGACGTCAA  TGGGTGGACT
GGTTGCTGGG  GGCGGGTAAC  TGCAGTTATT  ACTGCATACA  AGGGTATCAT  TGCGGTTATC  CCTGAAAGGT  AACTGCAGTT  ACCCACCTGA

       550         560         570         580         590         600         610         620         630
ATTTACGGTA  AACTGCCCAC  TTGGCAGTAC  ATCAAGTGTA  TCATATGCCA  AGTACGCCCC  CTATTGACGT  CAATGACGGT  AAATGGCCCG
TAAATGCCAT  TTGACGGGTG  AACCGTCATG  TAGTTCACAT  AGTATACGGT  TCATGCGGGG  GATAACTGCA  GTTACTGCCA  TTTACCGGGC

       640         650         660         670         680         690         700         710         720
CCTGGCATTA  TGCCCAGTAC  ATGACCTTAT  GGGACTTTCC  TACTTGGCAG  TACATCTACG  TATTAGTCAT  CGCTATTACC  ATGGTGATGC
GGACCGTAAT  ACGGGTCATG  TACTGGAATA  CCCTGAAAGG  ATGAACCGTC  ATGTAGATGC  ATAATCAGTA  GCGATAATGG  TACCACTACG

       730         740         750         760         770         780         790         800         810
GGTTTTGGCA  GTACATCAAT  GGGCGTGGAT  AGCGGTTTGA  CTCACGGGGA  TTTCCAAGTC  TCCACCCCAT  TGACGTCAAT  GGGAGTTTGT
CCAAAACCGT  CATGTAGTTA  CCCGCACCTA  TCGCCAAACT  GAGTGCCCCT  AAAGGTTCAG  AGGTGGGGTA  ACTGCAGTTA  CCCTCAAACA

       820         830         840         850         860         870         880         890         900
TTTGGCACCA  AAATCAACGG  GACTTTCCAA  AATGTCGTAA  CAACTCCGCC  CCATTGACGC  AAATGGGCCG  TAGGCGTGTA  CGGTGGGAGG
AAACCGTGGT  TTTAGTTGCC  CTGAAAGGTT  TTACAGCATT  GTTGAGGCGG  GGTAACTGCG  TTTACCCGGC  ATCCGCACAT  GCCACCCTCC
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FIGURE 14A
(SEQ ID NO. 10)

pD17-cJ-dCH2.H1

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      910        920        930        940        950        960        970        980        990
TCTATATAAG CAGAGCTCTC TGGCTAACTA GAGAACCCAC TGCTTACTGG CTTATCGAAA TTAATACGAC TCACTATAGG GAGACCCAAG
AGATATATTC GTCTCGAGAG ACCGATTGAT CTCTTGGGTG ACGAATGACC GAATAGCTTT AATTATGCTG AGTGATATCC CTCTGGGTTC

     1000       1010       1020       1030       1040       1050       1060       1070       1080
CTTGGTACCA ATTTAAATTG ATATCTCCTT AGGTCTCGAG TCTCTAGATA ACCGGTCAAT CGATTGGAAT TCTTGCGGCC GCTTGCTAGC
GAACCATGGT TAAATTTAAC TATAGAGGAA TCCAGAGCTC AGAGATCTAT TGGCCAGTTA GCTAACCCTA AGAACGCCGG CGAACGATCG

     1090       1100       1110       1120       1130       1140       1150       1160       1170
CACCATGGAG TTGTGGTTAA GCTTGGTCCT TCCTTGTCCT TGTTTTAAAA GGTGTCCAGT GTGAAGTGAA TCTGGTGGAG TCTGGGGGAG
GTGGTACCTC AACACCAATT CGAACCAGGA AGGAACAGGA ACAAAAATTT CCACAGGTCA CACTTCACTT AGACCACCTC AGACCCCCTC

     1180       1190       1200       1210       1220       1230       1240       1250       1260
GCTTAGTGCA GCCTGGAGGG TCCCTGAAAG TCTCCCTGTGT AACCCTCTGA TTCACTTTCA GTGACTATTA CATGTATTGG GTTCGCCAGA
CGAATCACGT CGGACCTCCC AGGGACTTTC AGAGGACACA TTGGAGACCT AAGTGAAAGT CACTGATAAT GTACATAACC CAAGCGGTCT

     1270       1280       1290       1300       1310       1320       1330       1340       1350
CTCCAGAGAA TGGGCTGGAG ACATTAGTCA AGGTGGTGAT ATAACCGACT ATCCAGACAC TGTAAAGGGT CGATTCACCA
GAGGTCTCTT CTCCGACCTC TGTAATCAGT TCCACCACTA TATTGGCTGA TAGGTCTGTG ACATTTCCCA GCTAAGTGGT

     1360       1370       1380       1390       1400       1410       1420       1430       1440
TCTCCAGAGA CAATGCCAAG AACACCCTGT ACCTGCAAAT GAGCCGTCTG AAGTCTGAGG ACACAGCCAT GTATTACTGT GCAAGAGGCC
AGAGGTCTCT GTTACGGTTC TTGTGGGACA TGGACGTTTA CTCGGCAGAC TTCAGACTCC TGTGTCGGTA CATAATGACA CGTTCTCCGG

     1450       1460       1470       1480       1490       1500       1510       1520       1530
TGGACGACGG GGCCTGGTTT GCTTACTGGG GCCAAGGGAC TCTGGTCACG GTCTCTGTAG CTAGCACCAA GGGCCCATCG GTCTTCCCCC
ACCTGCTGCC CCGGACCAAA CGAATGACCC CGGTTCCCTG AGACCAGTGC CAGAGACATC GATCGTGGTT CCCGGGTAGC CAGAAGGGGG

     1540       1550       1560       1570       1580       1590       1600       1610       1620
TGGCACCCTC CTCCAAGAGC ACCTCTGGGG GCACAGCGGC CCTGGGCTGC ACTACTTCCC CGAACCGGTG ACGGTGTCGT
ACCGTGGGAG GAGGTTCTCG TGGAGACCCC CGTGTCGCCG GGACCCGACG TGATGAAGGG GCTTGGCCAC TGCCACAGCA

     1630       1640       1650       1660       1670       1680       1690       1700       1710
GGAACTCAGG CGCCCTGACC AGCGGCGTGC ACACCTTCCC GGCTGTCCTA CAGTCCTCAG GACTCTACTC CCTCAGCAGC GTGGTCACCG
CCTTGAGTCC GCGGGACTGG TCGCCGCACG TGTGGAAGGG CCGACAGGAT GTCAGGAGTC CTGAGATGAG GGAGTCGTCG CACCAGTGGC

     1720       1730       1740       1750       1760       1770       1780       1790       1800
TGCCCTCCAG CAGCTTGGGC ACCCAGACCT ACATCTGCAA CGTGAATCAC AAGCCCAGCA ACACCAAGGT GGACAAGAAA GTTGGTGAGA
ACGGGAGGTC GTCGAACCCG TGGGTCTGGA TGTAGACGTT GCACTTAGTG TTCGGGTCGT TGTGGTTCCA CCTGTTCTTT CAACCACTCT
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FIGURE 14B
(SEQ ID NO. 10)

pD17-cJ-dCH2.H1

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      1810       1820       1830       1840       1850       1860       1870       1880       1890
GGCCAGCACA GGGAGGGAGG GTGTCTGCTG GAAGCCAGGC TCAGGCGCTCC TGCCTGGACG CATCCCGGCT ATGCAGCCCC AGTCCAGGGC
CCGGTCGTGT CCCTCCCTCC CACAGACGAC CTTCGGTCCG AGTCGGCGAGG ACGGACCTGC GTAGGGCCGA TACGTCGGGG TCAGGTCCCG

      1900       1910       1920       1930       1940       1950       1960       1970       1980
AGCAAGGCAG GCCCCGTCTG CCTCTTCACC CGGAGGCCTC TGCCCGCCCC ACTTCATGCTC AGGGAGAGGG TCTTCTGGCT TTTTCCCCAG
TCGTTCCGTC CGGGGCAGAC GGAGAAGTGG GCCTCCGGAG ACGGGCGGGG TGAGTACGAG TCCCTCTCCC AGAAGACCGA AAAAGGGGTC

      1990       2000       2010       2020       2030       2040       2050       2060       2070
GCTCTGGGCA GGCACAGGCT AGGTGCCCCT AACCCAGGCC CTGCACACAA AGGGGCAGGT GCTGGGCTCA GACCTGCCAA GAGCCATATC
CGAGACCCGT CCGTGTCCGA TCCACGGGGA TTGGGTCCGG GACGTGTGTT TCCCCGTCCA CGACCCGAGT CTGGACGGTT CTCGGTATAG

      2080       2090       2100       2110       2120       2130       2140       2150       2160
CGGGAGGACC CTGCCCCTGA CCTAAGCCCA CCCCAAAGGC CAAACTCTCC ACTCCCTCAG CTCGGACACC TTCTCTCCTC CCAGATTCCA
GCCCTCCTGG GACGGGGACT GGATTCGGGT GGGGTTTCCG GTTTGAGAGG TGAGGGAGTC GAGCCTGTGG AAGAGAGGAG GGTCTAAGGT

      2170       2180       2190       2200       2210       2220       2230       2240       2250
GTAACTCCCA ATCTTCTCTC TGCAGAGCCC AAATCTTGTG ACAAAACTCA CACATGCCCA CCGTGCCCAG GTAAGCCAGC CCAGGCCTCG
CATTGAGGGT TAGAAGAGAG ACGTCTCGGG TTTAGAACAC TGTTTTGAGT GTGTACGGGT GGCACGGGTC CATTCGGTCG GGTCCGGAGC

      2260       2270       2280       2290       2300       2310       2320       2330       2340
CCCTCCAGCT CAAGGCGGGA CAGGTGCCCT AGAGTAGCCT GCATCCAGGG ACACACCACG TGGGTACCAA CATGTCCGGA GCCACATGGA
GGGAGGTCGA GTTCCGCCCT GTCCACGGGA TCTCATCGGA CGTAGGTCCC TGTGTGGTGC ACCCATGGTT GTACAGGCCT CGGTGTACCT

      2350       2360       2370       2380       2390       2400       2410       2420       2430
CAGAGGCCGG CTCGGCCCAC CCTCTGCCCT GAGAGTGACC GCTGTACCAA CCTCTGTCCC TACAGGGCAG CCCCGAGAAC CACAGGTGTA
GTCTCCGGCC GAGCCGGGTG GGAGACGGGA CTCTCACTGG CGACATGGTT GGAGACAGGG ATGTCCCGTC GGGGCTCTTG GTGTCCACAT

      2440       2450       2460       2470       2480       2490       2500       2510       2520
CACCCTGCCC CCATCCCGGG ATGAGCTGAC CAAGAACCAG GTCAGCCTGA CCTGCCTGGT CAAAGGCTTC TATCCCAGCG ACATCGCCGT
GTGGGACGGG GGTAGGGCCC TACTCGACTG GTTCTTGGTC CAGTCGGACT GGACGGACCA GTTTCCGAAG ATAGGGTCGC TGTAGCGGCA

      2530       2540       2550       2560       2570       2580       2590       2600       2610
GGAGTGGGAG AGCAATGGGC AGCCGGAGAA CAACTACAAG ACCACGCCTC CCGTGCTGGA CTCCGACGGC TCCTTCTTCC TCTACAGCAA
CCTCACCCTC TCGTTACCCG TCGGCCTCTT GTTGATGTTC TGGTGCGGAG GGCACGACCT GAGGCTGCCG AGGAGAAGG AGATGTCGTT

      2620       2630       2640       2650       2660       2670       2680       2690       2700
GCTCACCGTG GACAAGAGCA GGTGGCAGCA GGGGAACGTC TTCTCATGCT CCGTGATGCA TGAGGCTCTG CACAACCACT ACACGCAGAA
CGAGTGGCAC CTGTTCTCGT CCACCGTCGT CCCCTTGCAG AAGAGTACGA GGCACTACGT ACTCCGAGAC GTGTTGGTGA TGTGCGTCTT
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FIGURE 14C
(SEQ ID NO. 10)

pD17-cJ-dCH2.H1

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         2710        2720        2730        2740        2750        2760        2770        2780        2790
   GAGCCTCTCC  CTGTCTCCGG  GTAAATGAGT  GCGACGGCCG  GCAAGCCCCC  GCTCCCCGGG  CTCTCGCGGT  CGCACGAGGA  TGCTTGGCAC
   CTCGGAGAGG  GACAGAGGCC  CATTTACTCA  CGCTGCCGGC  CGTTCGGGGG  CGAGGGGCCC  GAGAGCGCCA  GCGTGCTCCT  ACGAACCGTG

         2800        2810        2820        2830        2840        2850        2860        2870        2880
   GTACCCCCTG  TACATACTTC  CCGGGGCGCC  AGCATGGAAA  TAAAGCACCC  AGCGGCTGCCC TGGGCCCCTG  CGAGACTGTG  ATGGTTCTTT
   CATGGGGGAC  ATGTATGAAG  GGCCCGCGGG  TCGTACCTTT  ATTTCGTNGG  TCGCGACGGG  ACCCGGGGAC  GCTCTGACAC  TACCAAGAAA

         2890        2900        2910        2920        2930        2940        2950        2960        2970
   CCACGGGGTCA GGCCGAGTCT  GAGGCCTGAG  TGGCATGAGG  GAGGCAGAGC  GGGTCCCACT  GTCCCCACAC  TGGCCCAGGC  TGTGCAGGTG
   GGTGCCCAGT  CCGGCTCAGA  CTCCGGACTC  ACCGTACTCC  CTCCGTCTCG  CCCAGGGTGA  CAGGGGTGTG  ACCGGGTCCG  ACACGTCCAC

         2980        2990        3000        3010        3020        3030        3040        3050        3060
   TGCCTGGGCC  CCCTAGGGTG  GGGCTCAGCC  AGGGGCTGCC  CTCGGCAGGG  TGGGGGATTT  GCCAGCGTGG  CCCTCCCTCC  AGCAGCACCT
   ACGGACCCGG  GGGATCCCAC  CCCGAGTCGG  TCCCCGACGG  GAGCCGTCCC  ACCCCCTAAA  CGGTCGCACC  GGGAGGGAGG  TCGTCGTTGA

         3070        3080        3090        3100        3110        3120        3130        3140        3150
   GCCCTGGGCT  GGGCCACGGG  AAGCCCTAGG  AGCCCCTGGG  GACAGACACA  CAGCCCCTGC  CTCTGTAGGA  GACTGTCCTG  TTCTGTGAGC
   CGGGACCCGA  CCCGGTGCCC  TTCGGGATCC  TCGGGGACCC  CTGTCTGTGT  GTCGGGGACG  GAGACATCCT  CTGACAGGAC  AAGACACTCG

         3160        3170        3180        3190        3200        3210        3220        3230        3240
   GCCCCTGTCC  TCCCGACCTC  CATGCCCACT  CGGGGGCATG  CCTAGTCCAT  GTGCGTAGGG  ACAGGCCCTC  CCTCACCCAT  CTACCCCCAC
   CGGGACAGG   AGGGCTGGAG  GTACGGGTGA  GCCCCCGTAC  GGATCAGGTA  CACGCATCCC  TGTCCGGGAG  GGAGTGGGTA  GATGGGGGTG

         3250        3260        3270        3280        3290        3300        3310        3320        3330
   GGCACTAACC  CCTGGCTGCC  CTGCCCAGCC  TCGCACCCGC  ATGGGGACAC  AACCGACTCC  GGGGACATGC  ACTCTCGGGC  CCTGTGGAGG
   CCGTGATTGG  GGACCGACGG  GACGGGTCGG  AGCGTGGGCG  TACCCCTGTG  TTGGCTGAGG  CCCCTGTACG  TGAGAGCCCG  GGACACCTCC

         3340        3350        3360        3370        3380        3390        3400        3410        3420
   GACTGGTGCA  GATGCCCACA  CACACACTCA  GCCCAGACCC  GTTCAACAAA  CCCCGCACTG  AGGTTGGCCG  GCCACACGGC  CACCACACAC
   CTGACCACGT  CTACGGGTGT  GTGTGTGAGT  CGGGTCTGGG  CAAGTTGTTT  GGGGCGTGAC  TCCAACGGC   CGGTGTGCCG  GTGGTGTGTG

         3430        3440        3450        3460        3470        3480        3490        3500        3510
   ACACGTGCAC  GCCTCACACA  CGGAGCCTCA  CCCGGGCGAA  CTGCACAGCA  CCCAGACCAG  AGCAAGGTCC  TCGCACACGT  GAACACTCCT
   TGTGCACGTG  CGGAGTGTGT  GCCTCGGAGT  GGGCCCGCTT  GACGTGTCGT  GGGTCTGGTC  TCGTTCCAGG  AGCGTGTGCA  CTTGTGAGGA

         3520        3530        3540        3550        3560        3570        3580        3590        3600
   CGGACACAGG  CCCCACGCGG  CACCTCAAGG  CCCACGAGCC  TCTCGGCAGC  TTCTCCACAT  GCTGACCTGC  TCAGACAAAC
   GCCTGTGTCC  GGGGTGCGCC  GTGGAGTTCC  GGGTGCTCGG  AGAGCCGTCG  AAGAGGTGTA  CGACTGGACG  AGTCTGTTTG
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FIGURE 14D
(SEQ ID NO. 10)

pD17-cJ-dCH2.H1

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        3610       3620       3630       3640       3650       3660       3670       3680       3690
  CCAGCCCTCC TCTCACAAGG GTGCCCCTGC AGCCGCCACA CACACACAGG GGATCACACA CCACGTCACG TCCCTGGCCC TGGCCCACTT
  GGTCGGGAGG AGAGTGTTCC CACGGGGACG TCGGCGGTGT GTGTGTGTCC CCTAGTGTGT GGTGCAGTGC AGGGACCGGG ACCGGGTGAA

        3700       3710       3720       3730       3740       3750       3760       3770       3780
  CCCAGTGCCG CCCTTCCCTG CAGGACGGAT CAGCCTCGAC TGTGCCTTCT AGTTGCCAGC CATCTGTTGT TTGCCCCTCC CCCGTGCCTT
  GGGTCACGGC GGGAAGGGAC GTCCTGCCTA GTCGGAGCTG ACACGGAAGA TCAACGGTCG GTAGACAACA AACGGGGAGG GGGCACGGAA

        3790       3800       3810       3820       3830       3840       3850       3860       3870
  CCTTGACCCT GGAAGGTGCC ACTCCCACTG TCCTTTCCTA ATAAAATGAG GAAATTGCAT CGCATTGCAT GAGTAGGTGT CATTCTATTC
  GGAACTGGGA CCTTCCACGG TGAGGGTGAC AGGAAAGGAT TATTTTACTC CTTTAACGTA GCGTAACGTA CTCATCCACA GTAAGATAAG

        3880       3890       3900       3910       3920       3930       3940       3950       3960
  TGGGGGGTGG GGTGGGGCAG GACAGCAAGG GGGAGGATTG GGAAGACAAT AGCAGGCATG CTGGGGATGC GGTGGGCTCT ATGGCTTCTG
  ACCCCCCACC CCACCCCGTC CTGTCGTTCC CCCTCCTAAC CCTTCTGTTA TCGTCCGTAC GACCCCTACG CCACCCGAGA TACCGAAGAC

        3970       3980       3990       4000       4010       4020       4030       4040       4050
  AGGCGGAAAG AACCAGCTGG GGCTCTAGGG GGTATCCCCA CGCGCCCTGT AGCGGCGCAT TAAGCGCGGC GGGTGTGGTG GTTACGCCCA
  TCCGCCTTTC TTGGTCGACC CCGAGATCCC CCATAGGGGT GCGCGGGACA TCGCCGCGTA ATTCGCGCCG CCCACACCAC CAATGCGGGT

        4060       4070       4080       4090       4100       4110       4120       4130       4140
  GCGTGACCGC TACACTTGCC AGCGCCCTAG CGCCGCCTCC TTTCGCTTTC TTCCCTTCCT TTCTCGGCAC GTTCGCGGGG CCTCTCAAAA
  CGCACTGGCG ATGTGAACGG TCGCGGGATC GCGGCGGAGG AAAGCGAAAG AAGGGAAGGA AAGAGCCGTG CAAGCGCCCC GGAGAGTTTT

        4150       4160       4170       4180       4190       4200       4210       4220       4230
  AAGGGAAAAA AAGCATGCAT CTCAATTAGT CAGCAACCAT AGTCCCGCCC CTAACTCCGC CCTAACTCCG CCCAGTTCCG CCCAGTTCCG
  TTCCCTTTTT TTCGTACGTA GAGTTAATCA GTCGTTGGTA TCAGGGCGGG GATTGAGGCG GGATTGAGGC GGGTCAAGGC GGGTCAAGGC

        4240       4250       4260       4270       4280       4290       4300       4310       4320
  CCCATTCTCC GCCCCATGGC TGACTAATTT TTTTATTTA  TGCAGAGGCC GAGGCCGCCT CGGCCTCTGA GCTATTCCAG AAGTAGTGAG
  GGGTAAGAGG CGGGGTACCG ACTGATTAAA AAAATAAAT  ACGTCTCCGG CTCCGGCGGA GCCGGAGACT CGATAAGGTC TTCATCACTC

        4330       4340       4350       4360       4370       4380       4390       4400       4410
  GAGGCTTTTT TGGAGGCCTA AAAAGCTTGC ACAGCTCAGG GCTGCGATTT CGGCCAAAC  TTGACGGCAA           TCCTAGCGTG
  CTCCGAAAAA ACCTCCGGAT TTTTCGAACG TGTCGAGTCC CGACGCTAAA GCCGGTTTG  AACTGCCGTT           AGGATCGCAC

        4420       4430       4440       4450       4460       4470       4480       4490       4500
  AAGGCTGGTA GGATTTTATC CCCGCTGCCA TCATGGTTCG ACCATTGAAC TGCATCGTCG CCGTGTCCCA AAATATGGGG ATTGGCAAGA
  TTCCGACCAT CCTAAAATAG GGGCGACGGT AGTACCAAGC TGGTAACTTG ACGTAGCAGC GGCACAGGGT TTTATACCCC TAACCGTTCT
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FIGURE 14E
(SEQ ID NO. 10)

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          4510       4520       4530       4540       4550       4560       4570       4580       4590
     ACCGGAGACCT ACCCTGCCCT CCGCTCAGGA ACGAGTTCAA GTACTTCCAA AGAATGACCA CAACCTCTTC AGTGGAAGGT AAACAGAATC
     TGCCTCTCGGA TGGGACCGGA GGCGAGTCCT TGCTCAAGTT CATGAAGGTT TCTTACTGGT GTTGGAGAAG TCACCTTCCA TTTGTCTTAG

          4600       4610       4620       4630       4640       4650       4660       4670       4680
     TGGTGATTAT GGGTAGGAAA ACCTGGTTCT CCATTCCTGA GAAGAATCGA CCTTTAAAGG ACAGAATTAA TATAGTTCTC AGTAGAGAAC
     ACCACTAATA CCCATCCTTT TGGACCAAGA GGTAAGGACT CTTCTTAGCT GGAAATTTCC TGTCTTAATT ATATCAAGAG TCATCTCTTG

          4690       4700       4710       4720       4730       4740       4750       4760       4770
     TCAAAGAACC ACCACGAGGA GCTCATTTTC TTGCCAAAAG TTTGGATGAT GCCTTAAGAC TTATTGAACA ACCGGAATTG GCAAGTAAAG
     AGTTTCTTGG TGGTGCTCCT CGAGTAAAAG AACGGTTTTC AAACCTACTA CGGAATTCTG AATAACTTGT TGGCCTTAAC CGTTCATTTC

          4780       4790       4800       4810       4820       4830       4840       4850       4860
     TAGACATGGT TTGGATAGTC GGAGGCAGTT CTGTTTACCA GGAAGCCATG AATCAACCAG GCCACCTTAG ACTCTTTGTG ACAAGGATCA
     ATCTGTACCA AACCTATCAG CCTCCGTCAA GACAAATGGT CCTTCGGTAC TTAGTTGGTC CGGTGGAATC TGAGAAACAC TGTTCCTAGT

          4870       4880       4890       4900       4910       4920       4930       4940       4950
     TGCAGGAATT TGAAAGTGAC ACGTTTTTCC CAGAAATTGA TTTGGGGAAA TATAAACTTC TCCCAGAATA CCCAGCCGTC CTCTCTGAGG
     ACGTCCTTAA ACTTTCACTG TGCAAAAAGG GTCTTTAACT AAACCCCTTT ATATTTGAAG AGGGTCTTAT GGGTCCGCAG GAGAGACTCC

          4960       4970       4980       4990       5000       5010       5020       5030       5040
     TCCAGGAGGA AAAAGGCATC AAGTATAAGT TTGAAGTCTA CGAGAAGAAA GACTAACAGG AAGATGCTTT CAAGTTCTCT GCTCCCCTCC
     AGGTCCTCCT TTTTCCGTAG TTCATATTCA AACTTCAGAT GCTCTTCTTT CTGATTGTCC TTCTACGAAA GTTCAAGAGA CGAGGGGAGG

          5050       5060       5070       5080       5090       5100       5110       5120       5130
     TAAAGCTATG CATTTTTATA AGACCATGGG ACTTTTGCTG GCTTTAGATC TCTTTGTGAA GGAACCTTAC TTCTGTGGTG TGACATAATT
     ATTTCGATAC GTAAAAATAT TCTGGTACCC TGAAAACGAC CGAAATCTAG AGAAACACTT CCTTGGAATG AAGACACCAC ACTGTATTAA

          5140       5150       5160       5170       5180       5190       5200       5210       5220
     GGACAAACTA CCTACAGAGA TTTAAAGCTC TAAGGTAAAT ATAAAATTTT TAAGTGTATA ATGTGTTAAA CTACTGATTC TAATTGTTTG
     CCTGTTTGAT GGATGTCTCT AAATTTCGAG ATTCCATTTA TATTTTAAAA ATTCACATAT         GATGACTAAG ATTAACAAAC

          5230       5240       5250       5260       5270       5280       5290       5300       5310
     TGTATTTTAG ATTCCAACCT ATGGAACTGA TGAATGGGAG CAGTGGTGGA ATGCCTTTAA TGAGGAAAAC CTGTTTTGCT CAGAAGAAAT
     ACATAAAATC TAAGGTTGGA TACCTTGACT ACTTACCCTC GTCACCACCT TACGGAAATT ACTCCTTTTG GACAAAACGA GTCTTCTTTA

          5320       5330       5340       5350       5360       5370       5380       5390       5400
     GCCATCTAGT GATGATGAGG CTACTGCTGA CTCTCAACAT TCTACTCCTC CAAAAAAGAA GAGAAAGGTA GAAGACCCCA AGGACTTTCC
     CGGTAGATCA CTACTACTCC GATGACGACT GAGAGTTGTA AGATGAGGAG GTTTTTTCTT CTCTTTCCAT CTTCTGGGGT TCCTGAAAGG
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FIGURE 14F
(SEQ ID NO. 10)

pD17-cJ-dCH2.H1

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5410        5420        5430        5440        5450        5460        5470        5480        5490
TTCAGAAATTG CTAAGTTTTT TGAGTCATGC TGTGTTTAGT AATAGAACTC TTGCTTGCTT TGCTATTTAC ACCACAAAGG AAAAAGCTGC
AAGTCTTAAC  GATTCAAAAA ACTCAGTACG ACACAAATCA TTATCTTGAG AACGAACGAA ACGATAAATG TGGTGTTTCC TTTTTCGACG

5500        5510        5520        5530        5540        5550        5560        5570        5580
ACTGCTATAC  AAGAAAATTA TGGAAAAATA TTCTGTAACC TTTATAAGTA GGCATAACAG TTATAATCAT AACATACTGT TTTTTCTTAC
TGACGATATG  TTCTTTTTAT ACCTTTTTAT AAGACATTGG AAATATTCAT CCGTATTGTC AATATTAGTA TTGTATGACA AAAAAGAATG

5590        5600        5610        5620        5630        5640        5650        5660        5670
TCCACACAGG  CATAGAGTGT CTGCTATTAA TAACTATGCT CAAAAATTGT GTACCTTTAG CTTTTTAATT TGTAAAGGGG TTAATAAGGA
AGGTGTGTCC  GTATCTCACA GACGATAATT ATTGATACGA GTTTTTAACA CATGGAAATC GAAAAATTAA ACATTTCCCC AATTATTCCT

5680        5690        5700        5710        5720        5730        5740        5750        5760
ATATTTGATG  TATAGTGCCT TGACTAGAGA TCATAATCAG CCATACCACA TTTGTAGAGG TTTTACTTGC TTTAAAAAAC CTCCCACACC
TATAAACTAC  ATATCACGGA ACTGATCTCT AGTATTAGTC GGTATGGTGT AAACATCTCC AAAATGAACG AAATTTTTTG GAGGGTGTGG

5770        5780        5790        5800        5810        5820        5830        5840        5850
TCCCCCTGAA  AAAATGAATG CAATGTTGTT TGTTAACTTG TTTATTGCAG CTTATAATGG TTACAAATAA AGCAATAGCA 
AGGGGGACTT  TTTTACTTAC GTTAACAACA ACAATTGAAC AAATAACGTC GAATATTACC AATGTTTATT TCGTTATCGT 

5860        5870        5880        5890        5900        5910        5920        5930        5940
TCACAAATTT  CACAAATAAA GCATTTTTTT CACTGCATTC TAGTTGTGGT TTGTCCAAAC TCATCAATGT ATCTTATCAT GTCTCGATCG
AGTGTTTAAA  GTGTTTATTT CGTAAAAAAA GTGACGTAAG ATCAACACCA AACAGGTTTG AGTAGTTACA TAGAATAGTA CAGACCTAGC

5950        5960        5970        5980        5990        6000        6010        6020        6030
CCTCCAGCGC  GGGGATCTCA TGCTGGAGTT CTTCGCCCAC CCCAACTTGT TTATTGCAGC TTATAATGGT TTATAAATGGT TACAAATAAA
GGAGGTCGCG  CCCCTAGAGT ACGACCTCAA GAAGCGGGTG GGGTTGAACA AATAACGTCG AATATTACCA AATATTACCA ATGTTTATTT

6040        6050        6060        6070        6080        6090        6100        6110        6120
GCAATAGCAT  CACAAATTTC ACAAATAAAG CATTTTTTTC ACTGCATTCT AGTTGTGGTT TGTCCAAACT CATCAATGTA TCTTATCATG
CGTTATCGTA  GTGTTTAAAG TGTTTATTTC GTAAAAAAAG TGACGTAAGA TCAACACCAA ACAGGTTTGA GTAGTTACAT AGAATAGTAC

6130        6140        6150        6160        6170        6180        6190        6200        6210
TCTGTATACC  GTCGACCTCT AGCTAGAGCT TGGCGTAATC ATGGTCATAG CTGTTTCCTG TGTGAAATTG TTATCCGCTC ACAATTCCAC
AGACATATGG  CAGCTGGAGA TCGATCTCGA ACCGCATTAG TACCAGTATC GACAAAGGAC ACACTTTAAC AATAGGCGAG TGTTAAGGTG

6220        6230        6240        6250        6260        6270        6280        6290        6300
ACAACATACG  AGCCGGAAGC ATAAAGTGTA AAGCCTGGGG TGCCTAATGA GTGAGCTAAC TCACATTAAT TGCGTTGCGC TCACTGCCCG
TGTTGTATGC  TCGGCCTTCG TATTTCACAT TTCGGACCCC ACGGATTACT CACTCGATTG AGTGTAATTA ACGCAACGCG AGTGACGGGC
```

FIGURE 14G
(SEQ ID NO. 10)

pD17-cJ-dCH2.H1

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         6310       6320       6330       6340       6350       6360       6370       6380       6390
   CTTTCCAGTC GGGAAACCTG TCGTGCCAGC TGCATTAATG AATCGGCCAA CGCGCGGGGA GAGGCGGTTT GCGTATTGGG CGCTCTTCCG
   GAAAGGTCAG CCCTTTGGAC AGCACGGTCG ACGTAATTAC TTAGCCGGTT GCGCGCCCCT CTCCGCCAAA CGCATAACCC GCGAGAAGGC

         6400       6410       6420       6430       6440       6450       6460       6470       6480
   CTTCCTCGCT CACTGACTCG CTGCGCTCGG TCGTTCGGCT GCGGCGAGCG GTATCAGCTC ACTCAAAGGC GGTAATACGG TTATCCACAG
   GAAGGAGCGA GTGACTGAGC GACGCGAGCC AGCAAGCCGA CGCCGCTCGC CATAGTCGAG TGAGTTTCCG CCATTATGCC AATAGGTGTC

         6490       6500       6510       6520       6530       6540       6550       6560       6570
   AATCAGGGGA TAACGCAGGA AAGAACATGT GAGCAAAAGG CCAGCAAAAG GCCAGGAACC GTAAAAAGGC CGCGTTGCTG GCGTTTTTCC
   TTAGTCCCCT ATTGCGTCCT TTCTTGTACA CTCGTTTTCC GGTCGTTTTC CGGTCCTTGG CATTTTTCCG GCGCAACGAC CGCAAAAAGG

         6580       6590       6600       6610       6620       6630       6640       6650       6660
   ATAGGCTCCG CCCCCCTGAC GAGCATCACA AAAATCGACG CTCAAGTCAG AGGTGGCGAA ACCCGACAGG ACTATAAAGA TACCAGGCGT
   TATCCGAGGC GGGGGGACTG CTCGTAGTGT TTTTAGCTGC GAGTTCAGTC TCCACCGCTT TGGGCTGTCC TGATATTTCT ATGGTCCGCA

         6670       6680       6690       6700       6710       6720       6730       6740       6750
   TTCCCCCTGG AAGCTCCCTC GTGCGCTCTC CTGTTCCGAC CCTGCCGCTT ACCGGATACC TGTCCGCCTT TCTCCCTTCG GGAAGCGTGG
   AAGGGGGACC TTCGAGGGAG CACGCGAGAG GACAAGGCTG GGACGGCGAA TGGCCTATGG ACAGGCGGAA AGAGGGAAGC CCTTCGCACC

         6760       6770       6780       6790       6800       6810       6820       6830       6840
   CGCTTTCTCA ATGCTCACGC TGTAGGTATC TCAGTTCGGT GTAGGTCGTT CGCTCCAAGC TGGGCTGTGT GCACGAACCC CCCGTTCAGC
   GCGAAAGAGT TACGAGTGCG ACATCCATAG AGTCAAGCCA CATCCAGCAA GCGAGGTTCG ACCCGACACA CGTGCTTGGG GGGCAAGTCG

         6850       6860       6870       6880       6890       6900       6910       6920       6930
   CCGACCGCTG CGCCTTATCC GGTAACTATC GTCTTGAGTC CAACCCGGTA AGACACGACT TATCGCCACT GGCAGCAGCC ACTGGTAACA
   GGCTGGCGAC GCGGAATAGG CCATTGATAG CAGAACTCAG GTTGGGCCAT TCTGTGCTGA ATAGCGGTGA CCGTCGTCGG TGACCATTGT

         6940       6950       6960       6970       6980       6990       7000       7010       7020
   GGATTAGCAG AGCGAGGTAT GTAGGCGGTG CTACAGAGTT CTTGAAGTGG TGGCCTAACT ACGGCTACAC TAGAAGGACA GTATTTGGTA
   CCTAATCGTC TCGCTCCATA CATCCGCCAC GATGTCTCAA GAACTTCACC ACCGGATTGA TGCCGATGTG ATCTTCCTGT CATAAACCAT

         7030       7040       7050       7060       7070       7080       7090       7100       7110
   TCTGCGCTCT GCTGAAGCCA GTTACCTTCG GAAAAAGAGT TGGTAGCTCT TGATCCGGCA AACAAACCAC CGCTGGTAGC GGTGGTTTTT
   AGACGCGAGA CGACTTCGGT CAATGGAAGC CTTTTTCTCA ACCATCGAGA ACTAGGCCGT TTGTTTGGTG GCGACCATCG CCACCAAAAA

         7120       7130       7140       7150       7160       7170       7180       7190       7200
   TTGTTTGCAA GCAGCAGATT ACGCGCAGAA AAAAAGGATC TCAAGAAGAT CCTTTGATCT TTTCTACGGG GTCTGACGCT CAGTGGAACG
   AACAAACGTT CGTCGTCTAA TGCGCGTCTT TTTTTCCTAG AGTTCTTCTA GGAAACTAGA AAAGATGCCC CAGACTGCGA GTCACCTTGC
```

FIGURE 14H
(SEQ ID NO. 10)

pD17-cJ-dCH2.H1

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      7210       7220       7230       7240       7250       7260       7270       7280       7290
AAAACTCACG TTAAGGGATT TTGGTCATGA GATTATCAAA AAGGATCTTC ACCTAGATCC TTTAAAATTA AAAATGAAGT TTTAAATCAA
TTTTGAGTGC AATTCCCTAA AACCAGTACT CTAATAGTTT TTCCTAGAAG TGGATCTAGG AAATTTTAAT TTTTACTTCA AAATTTAGTT

      7300       7310       7320       7330       7340       7350       7360       7370       7380
TCTAAAGTAT ATATGAGTAA ACTTGGTCTG ACAGTTACCA ATGCTTAATC AGTGAGGCAC CTATCTCAGC TTTCGTTCAT AAAGCAAGTA
AGATTTCATA TATACTCATT TGAACCAGAC TGTCAATGGT TACGAATTAG TCACTCCGTG GATAGAGTCG CTAGACAGAT

      7390       7400       7410       7420       7430       7440       7450       7460       7470
CCATAGTTGC CTGACTCCCC GTCGTGTAGA TAACTACGAT ACGGGAGGGC TTACCATCTG GCCCCAGTGC TGCAATGATA CCGCGAGACC
GGTATCAACG GACTGAGGGG CAGCACATCT ATTGATGCTA TGCCCTCCCG AATGGTAGAC CGGGGTCACG ACGTTACTAT GGCGCTCTGG

      7480       7490       7500       7510       7520       7530       7540       7550       7560
CACGCTCACC GGCTCCAGAT TTATCAGCAA TAAACCAGCC AGCCGGAAGG GCCGAGCGCA GAAGTGGTCC TGCAACTTTA TCCGCCTCCA
GTGCGAGTGG CCGAGGTCTA AATAGTCGTT AATTGGTCGG TCGGCCTTCC CGGCTCGCGT CTTCACCAGG ACGTTGAAAT AGGCGGAGGT

      7570       7580       7590       7600       7610       7620       7630       7640       7650
TCCAGTCTAT TAATTGTTGC CGGGAAGCTA GAGTAAGTAG TTCGCCAGTT AATAGTTTGC GCAACGTTGT TGCCATTGCT ACAGGCATCG
AGGTCAGATA ATTAACAACG GCCCTTCGAT CTCATTCATC AAGCGGTCAA TTATCAAACG CGTTGCAACA ACGGTAACGA TGTCCGTAGC

      7660       7670       7680       7690       7700       7710       7720       7730       7740
TGGTGTCACG CTCGTCGTTT GGTATGGCTT CATTCAGCTC CGGTTCCCAA CGATCAAGGC GAGTTACATG ATCCCCCATG TTGTGCAAAA
ACCACAGTGC GAGCAGCAAA CCATACCGAA GTAAGTCGAG GCCAAGGGTT GCTAGTTCCG CTCAATGTAC TAGGGGGTAC AACACGTTTT

      7750       7760       7770       7780       7790       7800       7810       7820       7830
AAGCGGTTAG CTCCTTCGGT CCTCCGATCG TTGTCAGAAG TAAGTTGGCC GCAGTGTTAT CACTCATGGT TATGGCAGCA CTGCATAATT
TTCGCCAATC GAGGAAGCCA GGAGGCTAGC AACAGTCTTC ATTCAACCGG CGTCACAATA GTGAGTACCA ATACCGTCGT GACGTATTAA

      7840       7850       7860       7870       7880       7890       7900       7910       7920
CTCTTACTGT CATGCCATCC GTAAGATGCT TTTCTGTGAC TGGTGAGTAC TCAACCAAGT CATTCTGAGA ATAGTGTATG CGGCGACCGA
GAGAATGACA GTACGGTAGG CATTCTACGA AAAGACACTG ACCACTCATG AGTTGGTTCA GTAAGACTCT TATCACATAC GCCGCTGGCT

      7930       7940       7950       7960       7970       7980       7990       8000       8010
GTTGCTCTTG CCCGGCGTCA ATACGGGATA ATACCGCGCC ACATAGCAGA ACTTTAAAAG TGCTCATCAT TGGAAAACGT TCTTCGGGGC
CAACGAGAAC GGGCCGCAGT TATGCCCTAT TATGGGCGCG TGTATCGTCT TGAAATTTTC ACGAGTAGTA ACCTTTTGCA AGAAGCCCCG

      8020       8030       8040       8050       8060       8070       8080       8090       8100
GAAAACTCTC AAGGATCTTA CCGCTGTTGA GATCCAGTTC GATGTAACCC ACTCGTGCAC CCAACTGATC TTCAGCATCT TTTACTTTCA
CTTTTGAGAG TTCCTAGAAT GGCGACAACT CTAGGTCAAG CTACATTGGG TGAGCACGTG GGTTGACTAG AAGTCGTAGA AAATGAAAGT
```

FIGURE 14I
(SEQ ID NO. 10)

pD17-cJ-dCH2.H1

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          8110       8120       8130       8140       8150       8160       8170       8180       8190
CCAGCGTTYC TGGGTGAGCA AAAACAGGAA GGCAAAATGC CGCAAAAAAG GGAATAAGGG CGACACGGAA ATGTTGAATA CTCATACTCT
GGTCGCAAAG ACCCACTCGT TTTTGTCCTT CCGTTTTACG CGGTTTTTTC CCTTATTCCC GCTGTGCCTT TACAACTTAT GAGTATGAGA

          8200       8210       8220       8230       8240       8250       8260       8270       8280
TCCTTTTTCA ATATTATTGA AGCATTTATC AGGGTTATTG TCTCATGAGC GGATACATAT TTGAATGTAT TTAGAAAAAT AAACAAATAG
AGGAAAAAGT TATAATAACT TCGTAAATAG TCCCAATAAC AGAGTACTCG CCTATGTATA AACTTACATA AATCTTTTTA TTTGTTTATC

          8290       8300       8310       8320       8330
GGGTTCCGCG CACATTTCCC CGAAAAGTGC CACCTGACGT C
CCCAAGGCGC GTGTAAAGGG GCTTTTCACG GTGGACTGCA G
```

FIGURE 14J
SEQ ID NO. 10)

FIGURE 18A (SEQ ID NO. 22)

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   1  GGTACCAATT  TAAATTGATA  TCTCCTTAGG  TCTCGAGTCT  CTAGATAACC

  51  GGTCAATCGA  TTGGAATTCT  TGCGGCCGCT  TGCTAGCCAC  CATGGAGTTG

 101  TGGTTAAGCT  TGGTCTTCCT  TGTCCTTGTT  TTAAAAGGTG  TCCAGTGTGA

 151  AGTGCAACTG  GTGGAGTCTG  GGGGAGGCTT  AGTGCAGCCT  GGAGGGTCCC

 201  TGCGACTTTC  CTGTGCTGCA  TCTGGATTCC  CGTTCAGTGA  CTATTACATG

 251  TATTGGGTTC  GCCAGGCTCC  AGGCAAGGGA  CTGGAGTGGG  TCTCATACAT

 301  TAGTCAAGAT  GGTGATATAA  CCGACTATGC  AGACTCCGTA  AAGGGTCGAT

 351  TCACCATCTC  CAGAGACAAT  GCAAAGAACA  GCCTGTACCT  GCAAATGAAC

 401  AGCCTGAGGG  ACGAGGACAC  AGCCGTGTAT  TACTGTGCAA  GAGGCCTGGC

 451  GGACGGGGCC  TGGTTTGCTT  ACTGGGGCCA  AGGGACTCTG  GTCACGGTCT

 501  CTTCCGCTAG  CACCAAGGGC  CCATCGGTCT  TCCCCCTGGC  ACCCTCCTCC

 551  AAGAGCACCT  CTGGGGGCAC  AGCGGCCCTG  GGCTGCCTGG  TCAAGGACTA

 601  CTTCCCCGAA  CCGGTGACGG  TGTCGTGGAA  CTCAGGCGCC  CTGACCAGCG

 651  GCGTGCACAC  CTTCCCGGCT  GTCCTACAGT  CCTCAGGACT  CTACTCCCTC

 701  AGCAGCGTGG  TCACCGTGCC  CTCCAGCAGC  TTGGGCACCC  AGACCTACAT

 751  CTGCAACGTG  AATCACAAGC  CCAGCAACAC  CAAGGTGGAC  AAGAAAGTTG

 801  GTGAGAGGCC  AGCACAGGGA  GGGAGGGTGT  CTGCTGGAAG  CCAGGCTCAG

 851  CGCTCCTGCC  TGGACGCATC  CCGGCTATGC  AGCCCCAGTC  CAGGGCAGCA

 901  AGGCAGGCCC  CGTCTGCCTC  TTCACCCGGA  GGCCTCTGCC  CGCCCCACTC

 951  ATGCTCAGGG  AGAGGGTCTT  CTGGCTTTTT  CCCCAGGCTC  TGGGCAGGCA

1001  CAGGCTAGGT  GCCCCTAACC  CAGGCCCTGC  ACACAAAGGG  GCAGGTGCTG

1051  GGCTCAGACC  TGCCAAGAGC  CATATCCGGG  AGGACCCTGC. CCCTGACCTA

1101  AGCCCACCCC  AAAGGCCAAA  CTCTCCACTC  CCTCAGCTCG  GACACCTTCT

1151  CTCCTCCCAG  ATTCCAGTAA  CTCCCAATCT  TCTCTCTGCA  GAGCCCAAAT

1201  CTTGTGACAA  AACTCACACA  TGCCCACCGT  GCCCAGGTAA  GCCAGCCCAG

1251  GCCTCGCCCT  CCAGCTCAAG  GCGGGACAGG  TGCCCTAGAG  TAGCCTGCAT

1301  CCAGGGACAG  GCCCCAGCCG  GGTGCTGACA  CGTCCACCTC  CATCTCTTCC
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                         235      237
1351  TCAGCACCTG AACTCCTGGG GGGACCGTCA GTCTTCCTCT TCCCCCCAAA

1401  ACCCAAGGAC ACCCTCATGA TCTCCCGGAC CCCTGAGGTC ACATGCGTGG

1451  TGGTGGACGT GAGCCACGAA GACCCTGAGG TCAAGTTCAA CTGGTACGTG

1501  GACGGCGTGG AGGTGCATAA TGCCAAGACA AAGCCGCGGG AGGAGCAGTA

1551  CAACAGCACG TACCGTGTGG TCAGCGTCCT CACCGTCCTG CACCAGGACT
                         318       320    322
1601  GGCTGAATGG CAAGGAGTAC AAGTGCAAGG TCTCCAACAA AGCCCTCCCA
           331
1651  GCCCCCATCG AGAAAACCAT CTCCAAAGCC AAAGGTGGGA CCCGTGGGGT

1701  GCGAGGGCCA CATGGACAGA GGCCGGCTCG GCCCACCCTC TGCCCTGAGA

1751  GTGACCGCTG TACCAACCTC TGTCCCTACA GGGCAGCCCC GAGAACCACA

1801  GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG AACCAGGTCA

1851  GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG

1901  TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT

1951  GCTGGACTCC GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA

2001  AGAGCAGGTG GCAGCAGGGG AACGTCTTCT CATGCTCCGT GATGCATGAG

2051  GCTCTGCACA ACCACTACAC GCAGAAGAGC CTCTCCCTGT CTCCGGGTAA

2101  ATGAGTGCGA CGGCCGGCAA GCCCCCGCTC CCCGGGCTCT CGCGGTCGCA

2151  CGAGGATGCT TGGCACGTAC CCCCTGTACA TACTTCCCGG GCGCCCAGCA

2201  TGGAAATAAA GCACCCAGCG CTGCCCTGGG CCCCTGCGAG ACTGTGATGG

2251  TTCTTTCCAC GGGTCAGGCC GAGTCTGAGG CCTGAGTGGC ATGAGGGAGG

2301  CAGAGCGGGT CCCACTGTCC CCACACTGGC CCAGGCTGTG CAGGTGTGCC

2351  TGGGCCCCCT AGGGTGGGGC TCAGCCAGGG CTGCCCTCG GCAGGGTGGG

2401  GGATTTGCCA GCGTGGCCCT CCCTCCAGCA GCACCTGCCC TGGGCTGGGC

2451  CACGGGAAGC CCTAGGAGCC CCTGGGGACA GACACACAGC CCCTGCCTCT

2501  GTAGGAGACT GTCCTGTTCT GTGAGCGCCC CTGTCCTCCC GACCTCCATG

2551  CCCACTCGGG GGCATGCCTA GTCCATGTGC GTAGGGACAG GCCCTCCCTC

2601  ACCCATCTAC CCCCACGGCA CTAACCCCTG GCTGCCCTGC CCAGCCTCGC

2651  ACCCGCATGG GGACACAACC GACTCCGGGG ACATGCACTC TCGGGCCCTG

2701  TGGAGGGACT GGTGCAGATG CCCACACACA CACTCAGCCC AGACCCGTTC

2751  AACAAACCCC GCACTGAGGT TGGCCGGCCA CACGGCCACC ACACACACAC

2801  GTGCACGCCT CACACACGGA GCCTCACCCG GGCGAACTGC ACAGCACCCA
```

FIGURE 18B (SEQ ID NO. 22)

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2851   GACCAGAGCA AGGTCCTCGC ACACGTGAAC ACTCCTCGGA CACAGGCCCC

2901   CACGAGCCCC ACGCGGCACC TCAAGGCCCA CGAGCCTCTC GGCAGCTTCT

2951   CCACATGCTG ACCTGCTCAG ACAAACCCAG CCCTCCTCTC ACAAGGGTGC

3001   CCCTGCAGCC GCCACACACA CACAGGGGAT CACACACCAC GTCACGTCCC

3051   TGGCCCTGGC CCACTTCCCA GTGCCGCCCT TCCCTGCAGG ACGGATCAGC

3101   CTCGACTGTG CCTTCTAGTT GCCAGCCATC TGTTGTTTGC CCCTCCCCCG

3151   TGCCTTCCTT GACCCTGGAA GGTGCCACTC CCACTGTCCT TTCCTAATAA

3201   AATGAGGAAA TTGCATCGCA TTGTCTGAGT AGGTGTCATT CTATTCTGGG

3251   GGGTGGGGTG GGGCAGGACA GCAAGGGGGA GGATTGGGAA GACAATAGCA

3301   GGCATGCTGG GGATGCGGTG GGCTCTATGG CTTCTGAGGC GGAAAGAACC

3351   AGCTGGGGCT CTAGGGGGTA TCCCCACGCG CCCTGTAGCG GCGCATTAAG

3401   CGCGGCGGGT GTGGTGGTTA CGCGCAGCGT GACCGCTACA CTTGCCAGCG

3451   CCCTAGCGCC CGCTCCTTTC GCTTTCTTCC CTTCCTTTCT CGCCACGTTC

3501   GCCGGGCCTC TCAAAAAAGG GAAAAAAGC ATGCATCTCA ATTAGTCAGC

3551   AACCATAGTC CCGCCCCTAA CTCCGCCCAT CCCGCCCCTA ACTCCGCCCA

3601   GTTCCGCCCA TTCTCCGCCC CATGGCTGAC TAATTTTTTT TATTTATGCA

3651   GAGGCCGAGG CCGCCTCGGC CTCTGAGCTA TTCCAGAAGT AGTGAGGAGG

3701   CTTTTTTGGA GGCCTAGGCT TTTGCAAAAA GCTTGGACAG CTCAGGGCTG

3751   CGATTTCGCG CCAAACTTGA CGGCAATCCT AGCGTGAAGG CTGGTAGGAT

3801   TTTATCCCCG CTGCCATCAT GGTTCGACCA TTGAACTGCA TCGTCGCCGT

3851   GTCCCAAAAT ATGGGGATTG GCAAGAACGG AGACCTACCC TGGCCTCCGC

3901   TCAGGAACGA GTTCAAGTAC TTCCAAAGAA TGACCACAAC CTCTTCAGTG

3951   GAAGGTAAAC AGAATCTGGT GATTATGGGT AGGAAAACCT GGTTCTCCAT

4001   TCCTGAGAAG AATCGACCTT TAAAGGACAG AATTAATATA GTTCTCAGTA

4051   GAGAACTCAA AGAACCACCA CGAGGAGCTC ATTTTCTTGC CAAAAGTTTG

4101   GATGATGCCT TAAGACTTAT TGAACAACCG GAATTGGCAA GTAAAGTAGA

4151   CATGGTTTGG ATAGTCGGAG GCAGTTCTGT TTACCAGGAA GCCATGAATC

4201   AACCAGGCCA CCTTAGACTC TTTGTGACAA GGATCATGCA GGAATTTGAA

4251   AGTGACACGT TTTTCCCAGA AATTGATTTG GGGAAATATA AACTTCTCCC

4301   AGAATACCCA GGCGTCCTCT CTGAGGTCCA GGAGGAAAAA GGCATCAAGT
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FIGURE 18C (SEQ ID NO. 22)

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4351   ATAAGTTTGA AGTCTACGAG AAGAAAGACT AACAGGAAGA TGCTTTCAAG

4401   TTCTCTGCTC CCCTCCTAAA GCTATGCATT TTTATAAGAC CATGGGACTT

4451   TTGCTGGCTT TAGATCTCTT TGTGAAGGAA CCTTACTTCT GTGGTGTGAC

4501   ATAATTGGAC AAACTACCTA CAGAGATTTA AAGCTCTAAG GTAAATATAA

4551   AATTTTTAAG TGTATAATGT GTTAAACTAC TGATTCTAAT TGTTTGTGTA

4601   TTTTAGATTC CAACCTATGG AACTGATGAA TGGGAGCAGT GGTGGAATGC

4651   CTTTAATGAG GAAAACCTGT TTTGCTCAGA AGAAATGCCA TCTAGTGATG

4701   ATGAGGCTAC TGCTGACTCT CAACATTCTA CTCCTCCAAA AAAGAAGAGA

4751   AAGGTAGAAG ACCCCAAGGA CTTTCCTTCA GAATTGCTAA GTTTTTTGAG

4801   TCATGCTGTG TTTAGTAATA GAACTCTTGC TTGCTTTGCT ATTTACACCA

4851   CAAAGGAAAA AGCTGCACTG CTATACAAGA AAATTATGGA AAAATATTCT

4901   GTAACCTTTA TAAGTAGGCA TAACAGTTAT AATCATAACA TACTGTTTTT

4951   TCTTACTCCA CACAGGCATA GAGTGTCTGC TATTAATAAC TATGCTCAAA

5001   AATTGTGTAC CTTTAGCTTT TTAATTTGTA AAGGGGTTAA TAAGGAATAT

5051   TTGATGTATA GTGCCTTGAC TAGAGATCAT AATCAGCCAT ACCACATTTG

5101   TAGAGGTTTT ACTTGCTTTA AAAAACCTCC CACACCTCCC CCTGAACCTG

5151   AAACATAAAA TGAATGCAAT TGTTGTTGTT AACTTGTTTA TTGCAGCTTA

5201   TAATGGTTAC AAATAAAGCA ATAGCATCAC AAATTTCACA AATAAAGCAT

5251   TTTTTTCACT GCATTCTAGT TGTGGTTTGT CCAAACTCAT CAATGTATCT

5301   TATCATGTCT GGATCGGCTG GATGATCCTC CAGCGCGGGG ATCTCATGCT

5351   GGAGTTCTTC GCCCACCCCA ACTTGTTTAT TGCAGCTTAT AATGGTTACA

5401   AATAAAGCAA TAGCATCACA AATTTCACAA ATAAAGCATT TTTTTCACTG

5451   CATTCTAGTT GTGGTTTGTC CAAACTCATC AATGTATCTT ATCATGTCTG

5501   TATACCGTCG ACCTCTAGCT AGAGCTTGGC GTAATCATGG TCATAGCTGT

5551   TTCCTGTGTG AAATTGTTAT CCGCTCACAA TTCCACACAA CATACGAGCC

5601   GGAAGCATAA AGTGTAAAGC CTGGGGTGCC TAATGAGTGA GCTAACTCAC

5651   ATTAATTGCG TTGCGCTCAC TGCCCGCTTT CCAGTCGGGA AACCTGTCGT

5701   GCCAGCTGCA TTAATGAATC GGCCAACGCG CGGGGAGAGG CGGTTTGCGT

5751   ATTGGGCGCT CTTCCGCTTC CTCGCTCACT GACTCGCTGC GCTCGGTCGT

5801   TCGGCTGCGG CGAGCGGTAT CAGCTCACTC AAAGGCGGTA ATACGGTTAT
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<div align="center">

FIGURE 18D (SEQ ID NO. 22)

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5851    CCACAGAATC AGGGGATAAC GCAGGAAAGA ACATGTGAGC AAAAGGCCAG

5901    CAAAAGGCCA GGAACCGTAA AAAGGCCGCG TTGCTGGCGT TTTTCCATAG

5951    GCTCCGCCCC CCTGACGAGC ATCACAAAAA TCGACGCTCA AGTCAGAGGT

6001    GGCGAAACCC GACAGGACTA TAAAGATACC AGGCGTTTCC CCCTGGAAGC

6051    TCCCTCGTGC GCTCTCCTGT TCCGACCCTG CCGCTTACCG GATACCTGTC

6101    CGCCTTTCTC CCTTCGGGAA GCGTGGCGCT TTCTCAATGC TCACGCTGTA

6151    GGTATCTCAG TTCGGTGTAG GTCGTTCGCT CCAAGCTGGG CTGTGTGCAC

6201    GAACCCCCCG TTCAGCCCGA CCGCTGCGCC TTATCCGGTA ACTATCGTCT

6251    TGAGTCCAAC CCGGTAAGAC ACGACTTATC GCCACTGGCA GCAGCCACTG

6301    GTAACAGGAT TAGCAGAGCG AGGTATGTAG GCGGTGCTAC AGAGTTCTTG

6351    AAGTGGTGGC CTAACTACGG CTACACTAGA AGGACAGTAT TTGGTATCTG

6401    CGCTCTGCTG AAGCCAGTTA CCTTCGGAAA AAGAGTTGGT AGCTCTTGAT

6451    CCGGCAAACA AACCACCGCT GGTAGCGGTG GTTTTTTTGT TTGCAAGCAG

6501    CAGATTACGC GCAGAAAAAA AGGATCTCAA GAAGATCCTT TGATCTTTTC

6551    TACGGGGTCT GACGCTCAGT GGAACGAAAA CTCACGTTAA GGGATTTTGG

6601    TCATGAGATT ATCAAAAAGG ATCTTCACCT AGATCCTTTT AAATTAAAAA

6651    TGAAGTTTTA AATCAATCTA AAGTATATAT GAGTAAACTT GGTCTGACAG

6701    TTACCAATGC TTAATCAGTG AGGCACCTAT CTCAGCGATC TGTCTATTTC

6751    GTTCATCCAT AGTTGCCTGA CTCCCCGTCG TGTAGATAAC TACGATACGG

6801    GAGGGCTTAC CATCTGGCCC CAGTGCTGCA ATGATACCGC GAGACCCACG

6851    CTCACCGGCT CCAGATTTAT CAGCAATAAA CCAGCCAGCC GGAAGGGCCG

6901    AGCGCAGAAG TGGTCCTGCA ACTTTATCCG CCTCCATCCA GTCTATTAAT

6951    TGTTGCCGGG AAGCTAGAGT AAGTAGTTCG CCAGTTAATA GTTTGCGCAA

7001    CGTTGTTGCC ATTGCTACAG GCATCGTGGT GTCACGCTCG TCGTTTGGTA

7051    TGGCTTCATT CAGCTCCGGT TCCCAACGAT CAAGGCGAGT TACATGATCC

7101    CCCATGTTGT GCAAAAAGC GGTTAGCTCC TTCGGTCCTC CGATCGTTGT

7151    CAGAAGTAAG TTGGCCGCAG TGTTATCACT CATGGTTATG GCAGCACTGC

7201    ATAATTCTCT TACTGTCATG CCATCCGTAA GATGCTTTTC TGTGACTGGT

7251    GAGTACTCAA CCAAGTCATT CTGAGAATAG TGTATGCGGC GACCGAGTTG

7301    CTCTTGCCCG GCGTCAATAC GGGATAATAC CGCGCCACAT AGCAGAACTT
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FIGURE 18E (SEQ ID NO. 22)

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7351    TAAAAGTGCT CATCATTGGA AAACGTTCTT CGGGGCGAAA ACTCTCAAGG

7401    ATCTTACCGC TGTTGAGATC CAGTTCGATG TAACCCACTC GTGCACCCAA

7451    CTGATCTTCA GCATCTTTTA CTTTCACCAG CGTTCTGGG TGAGCAAAAA

7501    CAGGAAGGCA AAATGCCGCA AAAAAGGGAA TAAGGGCGAC ACGGAAATGT

7551    TGAATACTCA TACTCTTCCT TTTTCAATAT TATTGAAGCA TTTATCAGGG

7601    TTATTGTCTC ATGAGCGGAT ACATATTTGA ATGTATTTAG AAAAATAAAC

7651    AAATAGGGGT TCCGCGCACA TTTCCCCGAA AAGTGCCACC TGACGTCGAC

7701    GGATCGGGAG ATCTGCTAGG TGACCTGAGG CGCGCCGGCT TCGAATAGCC

7751    AGAGTAACCT TTTTTTTTAA TTTTATTTTA TTTTATTTTT GAGATGGAGT

7801    TTGGCGCCGA TCTCCCGATC CCCTATGGTC GACTCTCAGT ACAATCTGCT

7851    CTGATGCCGC ATAGTTAAGC CAGTATCTGC TCCCTGCTTG TGTGTTGGAG

7901    GTCGCTGAGT AGTGCGCGAG CAAAATTTAA GCTACAACAA GGCAAGGCTT

7951    GACCGACAAT TGCATGAAGA ATCTGCTTAG GGTTAGGCGT TTTGCGCTGC

8001    TTCGCGATGT ACGGGCCAGA TATACGCGTT GACATTGATT ATTGACTAGT

8051    TATTAATAGT AATCAATTAC GGGGTCATTA GTTCATAGCC CATATATGGA

8101    GTTCCGCGTT ACATAACTTA CGGTAAATGG CCCGCCTGGC TGACCGCCCA

8151    ACGACCCCCG CCCATTGACG TCAATAATGA CGTATGTTCC CATAGTAACG

8201    CCAATAGGGA CTTTCCATTG ACGTCAATGG GTGGACTATT TACGGTAAAC

8251    TGCCCACTTG GCAGTACATC AAGTGTATCA TATGCCAAGT ACGCCCCCTA

8301    TTGACGTCAA TGACGGTAAA TGGCCCGCCT GGCATTATGC CCAGTACATG

8351    ACCTTATGGG ACTTTCCTAC TTGGCAGTAC ATCTACGTAT TAGTCATCGC

8401    TATTACCATG GTGATGCGGT TTTGGCAGTA CATCAATGGG CGTGGATAGC

8451    GGTTTGACTC ACGGGGATTT CCAAGTCTCC ACCCCATTGA CGTCAATGGG

8501    AGTTTGTTTT GGCACCAAAA TCAACGGGAC TTTCCAAAAT GTCGTAACAA

8551    CTCCGCCCCA TTGACGCAAA TGGGCGGTAG GCGTGTACGG TGGGAGGTCT

8601    ATATAAGCAG AGCTCTCTGG CTAACTAGAG AACCCACTGC TTACTGGCTT

8651    ATCGAAATTA ATACGACTCA CTATAGGGAG ACCCAAGCTT
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FIGURE 18F (SEQ ID NO. 22)

FIGURE 19 A
(SEQ ID NO. 23)

pD17-hG1b

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          10         20         30         40         50         60
GGTACCAATT TAAATTGATA TCTCCTTAGG TCTCGAGTCT CTAGATAACC GGTCAATCGA
CCATGGTTAA ATTTAACTAT AGAGGAATCC AGAGCTCAGA GATCTATTGG CCAGTTAGCT

          70         80         90        100        110        120
TTGGAATTCT TGCGGCCGCT TGCTAGCACC AAGGGCCCAT CGGTCTTCCC CCTGGCACCC
AACCTTAAGA ACGCCGGCGA ACGATCGTGG TTCCCGGGTA GCCAGAAGGG GGACCGTGGG

         130        140        150        160        170        180
TCCTCCAAGA GCACCTCTGG GGGCACAGCG GCCCTGGGCT GCCTGGTCAA GGACTACTTC
AGGAGGTTCT CGTGGAGACC CCCGTGTCGC CGGGACCCGA CGGACCAGTT CCTGATGAAG

         190        200        210        220        230        240
CCCGAACCGG TGACGGTGTC GTGGAACTCA GGCGCCCTGA CCAGCGGCGT GCACACCTTC
GGGCTTGGCC ACTGCCACAG CACCTTGAGT CCGCGGGACT GGTCGCCGCA CGTGTGGAAG

         250        260        270        280        290        300
CCGGCTGTCC TACAGTCCTC AGGACTCTAC TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC
GGCCGACAGG ATGTCAGGAG TCCTGAGATG AGGGAGTCGT CGCACCAGTG GCACGGGAGG

         310        320        330        340        350        360
AGCAGCTTGG GCACCCAGAC CTACATCTGC AACGTGAATC ACAAGCCCAG CAACACCAAG
TCGTCGAACC CGTGGGTCTG GATGTAGACG TTGCACTTAG TGTTCGGGTC GTTGTGGTTC

         370        380        390        400        410        420
AGCAGCAAGA AAGTTGGTGA GAGGCCAGCA CAGGGAGGGA GGGTGTCTGC TGGAAGCCAG
TCGTCGTTCT TTCAACCACT CTCCGGTCGT GTCCCTCCCT CCCACAGACG ACCTTCGGTC

         430        440        450        460        470        480
GCTCAGCGCT CCTGCCTGGA CGCATCCCGG CTATGCAGCC CCAGTCCAGG GCAGCAAGGC
CGAGTCGCGA GGACGGACCT GCGTAGGGCC GATACGTCGG GGTCAGGTCC CGTCGTTCCG

         490        500        510        520        530        540
AGGCCCCGTC TGCCTCTTCA CCCGGAGGCC TCTGCCCGCC CCACTCATGC TCAGGGAGAG
TCCGGGGCAG ACGGAGAAGT GGGCCTCCGG AGACGGGCGG GGTGAGTACG AGTCCCTCTC

         550        560        570        580        590        600
GGTCTTCTGG CTTTTTCCCC AGGCTCTGGG CAGGCACAGG CTAGGTGCCC CTAACCCAGG
CCAGAAGACC GAAAAAGGGG TCCGAGACCC GTCCGTGTCC GATCCACGGG GATTGGGTCC
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FIGURE 19B
(SEQ ID NO. 23)

pD17-hG1b

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        610        620        630        640        650        660
CCCTGCACAC AAAGGGGCAG GTGCTGGGCT CAGACCTGCC AAGAGCCATA TCCGGGAGGA
GGGACGTGTG TTTCCCCGTC CACGACCCGA GTCTGGACGG TTCTCGGTAT AGGCCCTCCT

        670        680        690        700        710        720
CCCTGCCCCT GACCTAAGCC CACCCCAAAG GCCAAACTCT CCACTCCCTC AGCTCGGACA
GGGACGGGGA CTGGATTCGG GTGGGGTTTC CGGTTTGAGA GGTGAGGGAG TCGAGCCTGT

        730        740        750        760        770        780
CCTTCTCTCC TCCCAGATTC CAGTAACTCC CAATCTTCTC TCTGCAGAGC CCAAATCTTG
GGAAGAGAGG AGGGTCTAAG GTCATTGAGG GTTAGAAGAG AGACGTCTCG GGTTTAGAAC

        790        800        810        820        830        840
TGACAAAACT CACACATGCC CACCGTGCCC AGGTAAGCCA GCCCAGGCCT CGCCCTCCAG
ACTGTTTTGA GTGTGTACGG GTGGCACGGG TCCATTCGGT CGGGTCCGGA GCGGGAGGTC

        850        860        870        880        890        900
CTCAAGGCGG GACAGGTGCC CTAGAGTAGC CTGCATCCAG GGACAGGCCC CAGCCGGGTG
GAGTTCCGCC CTGTCCACGG GATCTCATCG GACGTAGGTC CCTGTCCGGG GTCGGCCCAC

        910        920        930        940     235 950 237 960
CTGACACGTC CACCTCCATC TCTTCCTCAG CACCTGAACT [CTGGGGGGA][CCGTCAGTCT
GACTGTGCAG GTGGAGGTAG AGAAGGAGTC GTGGACTTGA [GACCCCCCT][GGCAGTCAGA

        970        980        990        1000       1010       1020
TCCTCTTCCC CCCAAAAACC AAGGACACACC TCATGATCTC CCGGACCCCT GAGGTCACAT
AGGAGAAGGG GGGTTTTTGG TTCCTGTGGG AGTACTAGAG GGCCTGGGGA CTCCAGTGTA

        1030       1040       1050       1060       1070       1080
GCGTGGTGGT GGACGTGAGC CACGAAGACC CTGAGGTCAA GTTCAACTGG TACGTGGACG
CGCACCACCA CCTGCACTCG GTGCTTCTGG GACTCCAGTT CAAGTTGACC ATGCACCTGC

        1090       1100       1110       1120       1130       1140
GCGTGGAGGT GCATAATGCC AAGACAAAGC CGCGGGAGGA GCAGTACAAC AGCACGTACC
CGCACCTCCA CGTATTACGG TTCTGTTTCG GCGCCCTCCT CGTCATGTTG TCGTGCATGG

        1150       1160       1170       1180       1190 318 320 1200
GTCTGGTCAG CGTCCTCACC GTCCTGCACC AGGACTGGCT GAATGGCAAG GAGTACAAGT
CAGGACCAGTC GCAGGAGTGG CAGGACGTGG TCCTGACCGA CTTACCGTTC CTCATGTTCA
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FIGURE 19C
(SEQ ID NO. 23)

pD17-hG1b

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     322   1210        1220        1230  331(        1240        1250        1260
          GCAAGGTCTC  CAACAAAGCC  CTCCCAGCCC  CCATCGAGAA  AACCATCTCC  AAAGCCAAAG
          CGTTCCAGAG  GTTGTTTCGG  GAGGGTCGGG  GGTAGCTCTT  TTGGTAGAGG  TTTCGGTTTC

           1270        1280        1290        1300        1310        1320
          GTGGGACCCG  TGGGGTGCGA  GGGCCACATG  GACAGAGGCC  GGCTCGGCCC  ACCCTCTGCC
          CACCCTGGGC  ACCCCACGCT  CCCGGTGTAC  CTGTCTCCGG  CCGAGCCGGG  TGGGAGACGG

           1330        1340        1350        1360        1370        1380
          CTGAGAGTGA  CCGCTGTACC  AACCTCTGTC  CCTACAGGGC  AGCCCCGAGA  ACCACAGGTG
          GACTCTCACT  GGCGACATGG  TTGGAGACAG  GGATGTCCCG  TCGGGGCTCT  TGGTGTCCAC

           1390        1400        1410        1420        1430        1440
          TACACCCCTGC CCCCATCCCG  GGATGAGCTG  ACCAAGAACC  AGGTCAGCCT  GACCTGCCTG
          ATGTGGGGACG GGGGTAGGGC  CCTACTCGAC  TGGTTCTTGG  TCCAGTCGGA  CTGGACGGAC

           1450        1460        1470        1480        1490        1500
          GTCAAAGGCT  TCTATCCCAG  CGACATCGCC  GTGGAGTGGG  AGAGCAATGG  GCAGCCGGAG
          CAGTTTCCGA  AGATAGGGTC  GCTGTAGCGG  CACCTCACCC  TCTCGTTACC  CGTCGGCCTC

           1510        1520        1530        1540        1550        1560
          AACAACTACA  AGACCACGCC  TCCCGTGCTG  GACTCCGACG  GCTCCTTCTT  CCTCTACAGC
          TTGTTGATGT  TCTGGTGCGG  AGGGCACGAC  CTGAGGCTGC  CGAGGAAGAA  GGAGATGTCG

           1570        1580        1590        1600        1610        1620
          AAGCTCACCG  TGGACAAGAG  CAGGTGGCAG  CAGGGGAACG  TCTTCTCATG  CTCCGTGATG
          TTCGAGTGGC  ACCTGTTCTC  GTCCACCGTC  GTCCCCTTGC  AGAAGAGTAC  GAGGCACTAC

           1630        1640        1650        1660        1670        1680
          CATGAGGCTC  TGCACAACCA  CTACACGCAG  AAGAGCCTCT  CCCTGTCTCC  GGGTAAATGA
          GTACTCCGAG  ACGTGTTGGT  GATGTGCGTC  TTCTCGGAGA  GGGACAGAGG  CCCATTTACT

           1690        1700        1710        1720        1730        1740
          GTGCGACGGC  CGGCAAGCCC  CCGCTCCCCG  GGCTCTCGCG  GTCGCACGAG  GATGCTTGGC
          CACGCTGCCG  GCCGTTCGGG  GGCGAGGGGC  CCGAGAGCGC  CAGCGTGCTC  CTACGAACCG

           1750        1760        1770        1780        1790        1800
          ACGTACCCCC  TGTACATACT  TCCCGGGCGC  CCAGCATGGA  AATAAAGCAC  CCAGCGCTGC
          TGCATGGGGG  ACATGTATGA  AGGGCCCGCG  GGTCGTACCT  TTATTTCGTG  GGTCGCGACG
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FIGURE 19D
(SEQ ID NO. 23)

pD17-hG1b

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     1810                1820          1830         1840         1850         1860
CCTGGGCCCC TGCGAGACTG TGATGGTTCT TTCCACGGGT CAGGCCGAGT CTGAGGCCTG
GGACCCGGGG ACGCTCTGAC ACTACCAAGA AAGGTGCCCA GTCCGGCTCA GACTCCGGAC

     1870                1880          1890         1900         1910         1920
AGTGGCATGA GGGAGGCAGA GCGGGTCCCA CTGTCCCCAC ACTGGCCCAG GCTGTGCAGG
TCACCGTACT CCCTCCGTCT CGCCCAGGGT GACAGGGGTG TGACCGGGTC CGACACGTCC

     1930                1940          1950         1960         1970         1980
TGTGCCTGGG CCCCCTAGGG TGGGGCTCAG CCAGGGGCTG CCCTCGGCAG GGTGGGGGAT
ACACGGACCC GGGGGATCCC ACCCCGAGTC GGTCCCCGAC GGGAGCCGTC CCACCCCCTA

     1990                2000          2010         2020         2030         2040
TTGCCAGCGT GGCCCTCCCT CCAGCAGCAC CTGCCCTGGG CTGGGCCACG GGAAGCCCTA
AACGGTCGCA CCGGGAGGGA GGTCGTCGTG GACGGGACCC GACCCGGTGC CCTTCGGGAT

     2050                2060          2070         2080         2090         2100
GGAGCCCCTG GGGACAGACA CACAGCCCCT GCCTCTGTAG GAGACTGTCC TGTTCTGTGA
CCTCGGGGAC CCCTGTCTGT GTGTCGGGGA CGGAGACATC CTCTGACAGG ACAAGACACT

     2110                2120          2130         2140         2150         2160
GCGCCCCTGT CCTCCCGACC TCCATGCCCA CTCGGGGGCA CTCGGGGGCT GCGGTGGGCT
CGCGGGGACA GGAGGGCTGG AGGTACGGGT GAGCCCCCGT ACGACCCCTA CGCCACCCGA

     2170                2180          2190         2200         2210         2220
CTATGGCTTC TGAGGCGGAA AGAACCAGCT GGGGCTCTAG GGGGTATCCC CACGGCGCCCT
GATACCGAAG ACTCCGCCTT TCTTGGTCGA CCCCGAGATC CCCCATAGGG GTGCGCGGGA

     2230                2240          2250         2260         2270         2280
GTAGCGGCGC ATTAAGCGCG GCGGGTGTGG TGGTTACGCG CAGCCGTGACC GCTACACTTG
CATCGCCGCG TAATTCGCGC CGCCCACACC ACCAATGCGC GTCGCACTGG CGATGTGAAC

     2290                2300          2310         2320         2330         2340
CCAGCGCCCT AGCGCCCGCT CCTTTCGCTT TCTTCCCTTC CTTTCTCGCC ACGTTCGCCG
GGTCGCGGGA TCGCGGGCGA GGAAAGCGAA AGAAGGGAAG GAAAGAGCGG TGCAAGCGGC

     2350                2360          2370         2380         2390         2400
GCTTTCCCCG TCAAGCTCTA AATCGGGGGCA TCCCTTTAGG GTTCCGATTT AGTGCTTTAC
CGAAAGGGGC AGTTCGAGAT TTAGCCCCCGT AGGGAAATCC CAAGGCTAAA TCACGAAATG
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FIGURE 19E
(SEQ ID NO. 23)

pD17-hG1b

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      2410       2420       2430       2440       2450       2460
GGCACCTCGA CCCCAAAAAA CTTGATTAGG GTGATGGTTC ACGTAGTGGG CCATCGCCCT
CCGTGGAGCT GGGGTTTTTT GAACTAATCC CACTACCAAG TGCATCACCC GGTAGCGGGA

      2470       2480       2490       2500       2510       2520
GATAGACGGT TTTTCGCCCT TTGACGTTGG AGTCCACGTT CTTTAATAGT GGACTCTTGT
CTATCTGCCA AAAAGCGGGA AACTGCAACC TCAGGTGCAA GAAATTATCA CCTGAGAACA

      2530       2540       2550       2560       2570       2580
TCCAAACTGG AACAACACTC AACCCTATCT CGGTCTATTC TTTTGATTTA TAAGGGATTT
AGGTTTGACC TTGTTGTGAG TTGGGATAGA GCCAGATAAG AAAACTAAAT ATTCCCTAAA

      2590       2600       2610       2620       2630       2640
TGGGGATTTC GGCCTATTGG TTAAAAAATG AGCTGATTTA ACAAAAATTT AACGCGAATT
ACCCCTAAAG CCGGATAACC AATTTTTTAC TCGACTAAAT TGTTTTTAAA TTGCGCTTAA

      2650       2660       2670       2680       2690       2700
AATTCTGTGG AATGTGTGTC AGTTAGGGTG TGGAAAGTCC CCAGGCTCCC CAGGCAGGCA
TTAAGACACC TTACACACAG TCAATCCCAC ACCTTTCAGG GGTCCGAGGG GTCCGTCCGT

      2710       2720       2730       2740       2750       2760
GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAT AGTCCCGCCC CTAACTCCGC
CTTCATACGT TTCGTACGTA GAGTTAATCA GTCGTTGGTA TCAGGGCGGG GATTGAGGCG

      2770       2780       2790       2800       2810       2820
CCATCCCGCC CCTAACTCCG CCCAGTTCCG CCCATTCTCC GCCCCATGGC TGACTAATTT
GGTAGGGCGG GGATTGAGGC GGGTCAAGGC GGGTAAGAGG CGGGGTACCG ACTGATTAAA

      2830       2840       2850       2860       2870       2880
TTTTTATTTA TGCAGAGGCC GAGGCCGCCT CGGCCTCTGA GCTATTCCAG AAGTAGTGAG
AAAAATAAAT ACGTCTCCGG CTCCGGCGGA GCCGGAGACT CGATAAGGTC TTCATCACTC

      2890       2900       2910       2920       2930       2940
GAGGCTTTTT TGGAGGCCTA GGCTTTTGCA AAAAGCTTGG ACAGCTCAGG GCTGCGATTT
CTCCGAAAAA ACCTCCGGAT CCGAAAACGT TTTTCGAACC TGTCGAGTCC CGACGCTAAA

      2950       2960       2970       2980       2990       3000
CGCGCCAAAC TTGACGGCAA TCCTAGCGTG AAGGCTGGTA GGATTTTATC CCGCTGCCA
GCGCGGTTTG AACTGCCGTT AGGATCGCAC TTCCGACCAT CCTAAAATAG GGGCGACGGT
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FIGURE 19F

(SEQ ID NO. 23)

pD17-hG1b

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     3010       3020       3030       3040       3050       3060
TCATGGTTCG ACCATTGAAC TGCATCGTCG CCGTGTCCCA AAATATGGGG ATTGGCAAGA
AGTACCAAGC TGGTAACTTG ACGTAGCAGC GGCACAGGGT TTTATACCCC TAACCGTTCT

     3070       3080       3090       3100       3110       3120
ACGGAGACCT ACCCTGGCCT CCGCTCAGGA ACGAGTTCAA GTACTTCCAA AGAATGACCA
TGCCTCTGGA TGGGACCGGA GGCGAGTCCT TGCTCAAGTT CATGAAGGTT TCTTACTGGT

     3130       3140       3150       3160       3170       3180
CAACCTCTTC AGTGGAAGGT AAACAGAATC TGGTGATTAT GGGTAGGAAA ACCTGGTTCT
GTTGGAGAAG TCACCTTCCA TTTGTCTTAG ACCACTAATA CCCATCCTTT TGGACCAAGA

     3190       3200       3210       3220       3230       3240
CCATTCCTGA GAAGAATCGA CCTTTAAAGG ACAGAATTAA TATAGTTCTC AGTAGAGAAC
GGTAAGGACT CTTCTTAGCT GGAAATTTCC TGTCTTAATT ATATCAAGAG TCATCTCTTG

     3250       3260       3270       3280       3290       3300
TCAAAGAACC ACCACGAGGA GCTCATTTTC TTGCCAAAAG TTTGGATGAT GCCTTAAGAC
AGTTTCTTGG TGGTGCTCCT CGAGTAAAAG AACGGTTTTC AAACCTACTA CGGAATTCTG

     3310       3320       3330       3340       3350       3360
TTATTGAACA ACCGGAATTG GCAAGTAAAG TAGACATGGT TTGGATAGTC GGAGGCAGTT
AATAACTTGT TGGCCTTAAC CGTTCATTTC ATCTGTACCA AACCTATCAG CCTCCGTCAA

     3370       3380       3390       3400       3410       3420
CTGTTTTACCA GGAAGCCATG AATCAACCAG GCCACCTTAG ACTCTTTGTG ACAAGGATCA
GACAAATGGT CCTTCGGTAC TTAGTTGGTC CGGTGGAATC TGAGAAACAC TGTTCCTAGT

     3430       3440       3450       3460       3470       3480
TGCAGGAATT TGAAAGTGAC ACGTTTTTCC CAGAAATTGA TTTGGGGAAA TATAAACTTC
ACGTCCTTAA ACTTTCACTG TGCAAAAAGG GTCTTTAACT AAACCCCTTT ATATTTGAAG

     3490       3500       3510       3520       3530       3540
TCCCAGAATA CCCAGGCGTC CTCTCTGAGG TCCAGGAGGA AAAAGGCATC AAGTATAAGT
AGGGTCTTAT GGGTCCGCAG GAGAGACTCC AGGTCCTCCT TTTTCCGTAG TTCATATTCA

     3550       3560       3570       3580       3590       3600
TTGAAGTCTA CGAGAAGAAA GACTAACAGG AAGATGCTTT CAAGTTCTCT GCTCCCCTCC
AACTTCAGAT GCTCTTCTTT CTGATTGTCC TTCTACGAAA GTTCAAGAGA CGAGGGGAGG
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FIGURE 19G
(SEQ ID NO. 23)

pD17-hG1b

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       3610       3620       3630       3640       3650       3660
TAAAGCTATG CATTTTTATA AGACCATGGG ACTTTGCTG GCTTTAGATC TCTTTGTGAA
ATTTCGATAC GTAAAAATAT TCTGGTACCC TGAAAACGAC CGAAATCTAG AGAAACACTT

       3670       3680       3690       3700       3710       3720
GGAACCTTAC TTCTGTGGTG TGACATAATT GGACAAACTA CCTACAGAGA TTTAAAGCTC
CCTTGGAATG AAGACACCAC ACTGTATTAA CCTGTTTGAT GGATGTCTCT AAATTTCGAG

       3730       3740       3750       3760       3770       3780
TAAGGTAAAT ATAAAATTTT TAAGTGTATA ATGTGTTAAA CTACTGATTC TAATTGTTTG
ATTCCATTTA TATTTTAAAA ATTCACATAT TACACAATTT GATGACTAAG AATTAACAAAC

       3790       3800       3810       3820       3830       3840
TGTATTTTAG ATTCCAACCT ATGGAACTGA TGAATGGGAG CAGTGGTGGA ATGCCTTTAA
ACATAAAATC TAAGGTTGGA TACCTTGACT ACTTACCCTC GTCACCACCT TACGGAAATT

       3850       3860       3870       3880       3890       3900
TGAGGAAAAC CTGTTTTGCT CAGAAGAAAT GCCATCTAGT GATGATGAGG CTACTGCTGA
ACTCCTTTTG GACAAAACGA GTCTTCTTTA CGGTAGATCA CTACTACTCC GATGACGACT

       3910       3920       3930       3940       3950       3960
CTCTCAACAT TCTACTCCTC CAAAAAAGAA GAGAAAGGTA GAAGACCCCA AGGACTTTCC
GAGAGTTGTA AGATGAGGAG GTTTTTTCTT CTCTTTCCAT CTTCTGGGGT TCCTGAAAGG

       3970       3980       3990       4000       4010       4020
TTCAGAATTG CTAAGTTTTT TGAGTCATGC TGTGTTTAGT AATAGAACTC TTGCTTGCTT
AAGTCTTAAC GATTCAAAAA ACTCAGTACG ACACAAATCA TTATCTTGAG AACGAACGAA

       4030       4040       4050       4060       4070       4080
TGCTATTTAC ACCACAAAGG AAAAAGCTGC ACTGCTATAC AAGAAAAATTA TGGAAAAATA
ACGATAAATG TGGTGTTTCC TTTTTCGACG TGACGATATG TTCTTTTTAAT ACCTTTTTAT

       4090       4100       4110       4120       4130       4140
TTCTGTAACC TTTATAAGTA GGCATAACAG TTATAATCAT AACATACTGT TTTTTCTTAC
AAGACATTGG AAATATTCAT CCGTATTGTC AATATTAGTA TTGTATGACA AAAAAGAATG

       4150       4160       4170       4180       4190       4200
TCCACACAGG CATAGAGTGT CTGCTATTAA TAACTATGCT CAAAAAATTGT GTACCTTTAG
AGGTGTGTCC GTATCTCACA GACGATAATT ATTGATACGA GTTTTTAACA CATGGAAATC
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pD17-hG1b

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        4210      4220      4230      4240      4250      4260
CTTTTAATT TGTAAAGGGG TTAATAAGGA ATATTTGATG TATAGTGCCT TGACTAGAGA
GAAAAATTAA ACATTTCCCC AATTATTCCT TATAAACTAC ATATCACGGA ACTGATCTCT

        4270      4280      4290      4300      4310      4320
TCATAATCAG CCATACCACA TTTGTAGAGG TTTTACTTGC TTTAAAAAAC CTCCCACACC
AGTATTAGTC GGTATGGTGT AAACATCTCC AAAATGAACG AAATTTTTTG GAGGGTGTGG

        4330      4340      4350      4360      4370      4380
TCCCCCTGAA CCTGAAACAT AAAATGAATG CAATTGTTGT TGTTAACTTG TTTATTGCAG
AGGGGGACTT GGACTTTGTA TTTTACTTAC GTTAACAACA ACAATTGAAC AAATAACGTC

        4390      4400      4410      4420      4430      4440
CTTATAAATGG TTACAAATAA AGCAATAGCA TCACAAATTT CACAAATAAA GCATTTTTTT
GAATATTACC AATGTTTATT TCGTTATCGT AGTGTTTAAA GTGTTTATTT CGTAAAAAAA

        4450      4460      4470      4480      4490      4500
CACTGCATTC TAGTTGTTGGT TTGTCCAAAC TCATCAATGT ATCTTATCAT GTCTGGATCG
GTGACGTAAG ATCAACACCA AACAGGTTTG AGTAGTTACA TAGAATAGTA CAGACCTAGC

        4510      4520      4530      4540      4550      4560
GCTGGATGAT CCTCCAGCGC GGGGATCTCA TGCTGGAGTT CTTCGCCCAC CCCAACTTGT
CGACCTACTA GGAGGTCGCG CCCCTAGAGT ACGACCTCAA GAAGCGGGTG GGGTTGAACA

        4570      4580      4590      4600      4610      4620
TTATTGCAGC TTATAATGGT TACAAATAAA GCAATAGCAT CACAAATTTC ACAAATAAAG
AATAACGTCG AATATTACCA ATGTTTATTT CGTTATCGTA GTGTTTAAAG TGTTTATTTC

        4630      4640      4650      4660      4670      4680
CATTTTTTTC ACTGCATTCT AGTTGTGGTT TGTCCAAACT CATCAATGTA TCTTATCATG
GTAAAAAAAG TGACGTAAGA TCAACACCAA ACAGGTTTGA GTAGTTACAT AGAATAGTAC

        4690      4700      4710      4720      4730      4740
TCTGTATACC GTCGACCTCT AGCTAGAGCT TGGCGTAATC ATGGTCATAG CTGTTTCCTG
AGACATATGG CAGCTGGAGA TCGATCTCGA ACCGCATTAG TACCAGTATC GACAAAGGAC

        4750      4760      4770      4780      4790      4800
TGTGAAATTG TTATCCGCTC ACAATTCCAC ACAACATACG AGCCGGAAGC ATAAAGTGTA
ACACTTAAC AATAGGCCGAG TGTTAAGGTG TGTTGTATGC TCGGCCTTCG TATTTCACAT
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pD17-hG1b

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4810       4820       4830       4840       4850       4860
AAGCCTGGGG TGCCTAATGA GTGAGCTAAC TCACATTAAT TGCGTTGCGC TCACTGCCCG
TTCGGACCCC ACGGATTACT CACTCGATTG AGTGTAATTA ACGCAACGCG AGTGACGGGC

4870       4880       4890       4900       4910       4920
CTTTCCAGTC GGGAAACCTG TCGTGCCAGC TGCATTAATG AATCGGCCAA CGGCGGGGGA
GAAAGGTCAG CCCTTTGGAC AGCACGGTCG ACGTAATTAC TTAGCCGGTT GCCGCGCCCT

4930       4940       4950       4960       4970       4980
GAGGCGGTTT GCGTATTGGG CGCTCCTTCCG CTTCCTCGCT CACTGACTCG CTGCGCTCGG
CTCCGCCAAA CGCATAACCC GCGAGAAGGC GAAGGAGCGA GTGACTGAGC GACGCGAGCC

4990       5000       5010       5020       5030       5040
TCGTTCGGCT GCGGGCGAGCG GTATCAGCTC ACTCAAAGGC GGTAATACGG TTATCCACAG
AGCAAGCCGA CGCCGCTCGC CATAGTCGAG TGAGTTTCCG CCATTATGCC AATAGGTGTC

5050       5060       5070       5080       5090       5100
AATCAGGGGA TAACGCAGGA AAGAACATGT GAGCAAAAGG CCAGCAAAAG GCCAGGAACC
TTAGTCCCCT ATTGCGTCCT TTCTTGTACA CTCGTTTTCC GGTCGTTTTC CGGTCCTTGG

5110       5120       5130       5140       5150       5160
GTAAAAAGGC CGCGGTTGCTG GCGTTTTTCC ATAGGCTCCG CCCCCCTGAC GAGCATCACA
CATTTTTCCG GCGCAACGAC CGCAAAAAGG TATCCGAGGC GGGGGGACTG CTCGTAGTGT

5170       5180       5190       5200       5210       5220
AAAATCGACG CTCAAGTCAG AGGTGGCGAA ACCCGACAGG ACTATAAAGA TACCAGGCGT
TTTTAGCTGC GAGTTCAGTC TCCACCGCTT TGGGCTGTCC TGATATTTCT ATGGTCCGCA

5230       5240       5250       5260       5270       5280
TTCCCCCTGG AAGCTCCCTC GTGCGCTCTC CTGTTCCGAC CCTGCCGCTT ACCGGATACC
AAGGGGGACC TTCGAGGGAG CACGCGAGAG GACAAGGCTG GGACGGCGAA TGGCCTATGG

5290       5300       5310       5320       5330       5340
TTCCCCCCTT TCTCCCTTCG GGAAGCGTGG CGCTTTCTCA ATGCTCACGC TGTAGGTATC
AAGGGGGGAA AGAGGGAAGC CCTTCGCACC GCGAAAGAGT TACGAGTGCG ACATCCATAG

5350       5360       5370       5380       5390       5400
TGTCCGCCTT GTAGGTCGTT CGCTCCAAGC TGGGCTGTGT GCACGAACCC CCCGTTCAGC
ACAGGCGGAA CATCCAGCAA GCGAGGTTCG ACCCGACACA CGTGCTTGGG GGGCAAGTCG
```

pD17-hG1b

```
5410       5420       5430       5440       5450       5460
CCGACCGCTG CGCCTTATCC GGTAACTATC GTCTTGAGTC CAACCCGGTA AGACACGACT
GGCTGGCGAC GCGGAATAGG CCATTGATAG CAGAACTCAG GTTGGGCCAT TCTGTGCTGA

5470       5480       5490       5500       5510       5520
TATCGCCACT GGCAGCAGCC ACTGGTAACA GGATTAGCAG AGCGAGGTAT GTAGGCGGTG
ATAGCGGTGA CCGTCGTCGG TGACCATTGT CCTAATCGTC TCGCTCCATA CATCCGCCAC

5530       5540       5550       5560       5570       5580
CTACAGAGTT CTTGAAGTGG TGGCCTAACT ACGGCTACAC TAGAAGGACA GTATTTGGTA
GATGTCTCAA GAACTTCACC ACCGGATTGA TGCCGATGTG ATCTTCCTGT CATAAACCAT

5590       5600       5610       5620       5630       5640
TCTGCGCTCT GCTGAAGCCA GTTACCTTCG GAAAAAGAGT TGGTAGCTCT TGATCCGGCA
AGACGCGAGA CGACTTCGGT CAATGGAAGC CTTTTTCTCA ACCATCGAGA ACTAGGCCGT

5650       5660       5670       5680       5690       5700
AACAAACCAC CGCTGGTAGC GGTGGTTTTT TTGTTTGCAA GCAGCAGATT ACGGCGCAGAA
TTGTTTGGTG GCGACCATCG CCACCAAAAA AACAAACGTT CGTCGTCTAA TGCGCGTCTT

5710       5720       5730       5740       5750       5760
AAAAAGGATC TCAAGAAGAT CCTTTGATCT TTTCTACGGG GTCTGACGCT CAGTGGAACG
TTTTTCCTAG AGTTCTTCTA GGAAACTAGA AAAGATGCCC CAGACTGCGA GTCACCTTGC

5770       5780       5790       5800       5810       5820
AAAACTCACG TTAAGGGATT TTGGTCATGA GATTATCAAA AAGGATCTTC ACCTAGATCC
TTTTGAGTGC AATTCCCTAA AACCAGTACT CTAATAGTTT TTCCTAGAAG TGGATCTAGG

5830       5840       5850       5860       5870       5880
TTTAAATTA  AAAATGAAGT TTTAAATCAA TCTAAAGTAT ATATGAGTAA ACTTGGTCTG
AAAATTTAAT TTTTACTTCA AAATTTAGTT AGATTTCATA TATACTCATT TGAACCAGAC

5890       5900       5910       5920       5930       5940
ACAGTTACCA ATGCTTAATC AGTGAGGCAC CTATCCTCAGC GATCTGTCTA TTTCGTTCAT
TGTCAATGGT TACGAATTAG TCACTCCGTG GATAGGAGTCG CTAGACAGAT AAAGCAAGTA

5950       5960       5970       5980       5990       6000
CCATAGTTGC CTGACTCCCC GTCGTGTAGA TAACTACGAT ACGGGAGGGC TTACCATCTG
GGTATCAACG GACTGAGGGG CAGCACATCT ATTGATGCTA TGCCCTCCCG AATGGTAGAC
```

FIGURE 19K
(SEQ ID NO. 23)

pD17-hG1b

```
      6010        6020        6030        6040        6050        6060
GCCCCAGTGC  TGCAATGATA  CCGGCGAGACC  CACGCTCACC  GGCTCCAGAT  TTATCAGCAA
CGGGGTCACG  ACGTTACTAT  GGCGCTCTGG   GTGCGAGTGG  CCGAGGTCTA  AATAGTCGTT

      6070        6080        6090        6100        6110        6120
TAAACCAGCC  AGCCGGAAGG  GCCGAGCGCA  GAAGTGGTCC  TGCAACTTTA  TCCGCCTCCA
ATTTGGTCGG  TCGGCCTTCC  CGGCTCGCGT  CTTCACCAGG  ACGTTGAAAT  AGGCGGAGGT

      6130        6140        6150        6160        6170        6180
TCCAGTCTAT  TAATTGTTGC  CGGGAAGCTA  GAGTAAGTAG  TTCGGCCAGTT  AATAGTTTGC
AGGTCAGATA  ATTAACAACG  GCCCTTCGAT  CTCATTCATC  AAGCGGTCAA  TTATCAAACG

      6190        6200        6210        6220        6230        6240
GCAACGTTGT  TGCCATTGCT  ACAGGCATCG  TGGTGTCACG  CTCGTCGTTT  GGTATGGCTT
CGTTGCAACA  ACGGTAACGA  TGTCCGTAGC  ACCACAGTGC  GAGCAGCAAA  CCATACCGAA

      6250        6260        6270        6280        6290        6300
CATTCAGCTC  CGGTTCCCAA  CGATCAAGGC  GAGTTACATG  ATCCCCCATG  TTGTGCAAAA
GTAAGTCGAG  GCCAAGGGTT  GCTAGTTCCG  CTCAATGTAC  TAGGGGGTAC  AACACGTTTT

      6310        6320        6330        6340        6350        6360
AAGCGGTTAG  CTCCTTCGGT  CCTCCGATCG  TTGTCAGAAG  TAAGTTGGCC  GCAGTGTTAT
TTCGCCAATC  GAGGAAGCCA  GGAGGCTAGC  AACAGTCTTC  ATTCAACCGG  CGTCACAATA

      6370        6380        6390        6400        6410        6420
CACTCATGGT  TATGGCAGCA  CTGCATAATT  CTCTTACTGT  CATGCCATCC  GTAAGATGCT
GTGAGTACCA  ATACCGTCGT  GACGTATTAA  GAGAATGACA  GTACGGTAGG  CATTCTACGA

      6430        6440        6450        6460        6470        6480
TTTCTGTGAC  TGGTGAGTAC  TCAACCAAGT  CATTCTGAGA  ATAGTGTATG  CGGCGACCGA
AAAGACACTG  ACCACTCATG  AGTTGGTTCA  GTAAGACTCT  TATCACATAC  GCCGCTGGCT

      6490        6500        6510        6520        6530        6540
GTTGCTCTTG  CCCGGGCGTCA  ATACGGGATA  ATACCGCGCC  ACATAGCAGA  ACTTTAAAAG
CAACGAGAAC  GGGCCGCAGT   TATGCCCTAT  TATGGCGCGG  TGTATCGTCT  TGAAATTTTC

      6550        6560        6570        6580        6590        6600
TGCTCATCAT  TGGAAAACGT  TCTTCGGGGC  GAAAACTCTC  AAGGATCTTA  CCGCTGTTGA
ACGAGTAGTA  ACCTTTTGCA  AGAAGCCCCG  CTTTTGAGAG  TTCCTAGAAT  GGCGACAACT
```

FIGURE 19L
(SEQ ID NO. 23)

pD17-hG1b

```
       6610         6620        6630        6640        6650        6660
GATCCCAGTTC  GATGTAACCC  ACTCGTGCAC  CCAACTGATC  TTCAGCATCT  TTTACTTTCA
CTAGGTCAAG   CTACATTGGG  TGAGCACGTG  GGTTGACTAG  AAGTCGTAGA  AAATGAAAGT

       6670         6680        6690        6700        6710        6720
CCAGCGTTTC   TGGGTGAGCA  AAAACAGGAA  GGCAAAATGC  CGCAAAAAAG  GGAATAAGGG
GGTCGCAAAG   ACCCACTCGT  TTTTGTCCTT  CCGTTTTACG  GCGTTTTTTC  CCTTATTCCC

       6730         6740        6750        6760        6770        6780
CGACACGGAA   ATGTTGAATA  CTCATACTCT  TCCTTTTTCA  ATATTATTGA  AGCATTTATC
GCTGTGCCTT   TACAACTTAT  GAGTATGAGA  AGGAAAAAGT  TATAATAACT  TCGTAAATAG

       6790         6800        6810        6820        6830        6840
AGGGTTATTG   TCTCATGAGC  GGATACATAT  TTGAATGTAT  TTAGAAAAAT  AAACAAATAG
TCCCAATAAC   AGAGTACTCG  CCTATGTATA  AACTTACATA  AATCTTTTTA  TTTGTTTATC

       6850         6860        6870        6880        6890        6900
GGGTTCCGCG   CACATTTCCC  CGAAAAGTGC  CACCTGACGT  CGACGGATCG  GGAGATCTGC
CCCAAGGCGC   GTGTAAAGGG  GCTTTTCACG  GTGGACTGCA  GCTGCCTAGC  CCTCTAGACG

       6910         6920        6930        6940        6950        6960
TAGGTGACCT   GAGGCCGCGCC GGCTTCGAAT  AGCCAGAGTA  ACCTTTTTTT  TTAATTTTAT
ATCCACTGGA   CTCCGCGCGG  CCGAAGCTTA  TCGGTCTCAT  TGGAAAAAAA  AATTAAAATA

       6970         6980        6990        7000        7010        7020
TTTATTTTAT   TTTTGAGATG  GAGTTTTGCG  CCGATCTCCC  GATCCCCTAT  GGTCGACTCT
AAATAAAATA   AAAACTCTAC  CTCAAAACGC  GGCTAGAGGG  CTAGGGGATA  CCAGCTGAGA

       7030         7040        7050        7060        7070        7080
CAGTACAATC   TGCTCTGATG  CCGCATAGTT  AAGCCAGTAT  CTGCTCCCTG  CTTGTGTGTT
GTCATGTTAG   ACGAGACTAC  GGCGTATCAA  TTCGGTCATA  GACGAGGGAC  GAACACACAA

       7090         7100        7110        7120        7130        7140
GGAGGTCGCT   GAGTAGTGCG  CGAGCAAAAT  TTAAGCTACA  ACAAGGCAAG  GCTTGACCGA
CCTCCAGCGA   CTCATCACGC  GCTCGTTTTA  AATTCGATGT  TGTTCCGTTC  CGAACTGGCT

       7150         7160        7170        7180        7190        7200
CAATTGCATG   AAGAATCTGC  TTAGGGTTAG  GCGTTTTGCG  CTGCTTCGCG  ATGTACGGGC
GTTAACGTAC   TTCTTAGACG  AATCCCAATC  CGCAAAACGC  GACGAAGCGC  TACATGCCCG
```

FIGURE 19M
(SEQ ID NO. 23)

pD17-hG1b

```
      7210            7220            7230            7240            7250            7260
CAGATATACG  CGTTGACATT  GATTATTGAC  TAGTTATTAA  TAGTAATCAA  TTACGGGGTC
GTCTATATGC  GCAACTGTAA  CTAATAACTG  ATCAATAATT  ATCATTAGTT  AATGCCCCAG

      7270            7280            7290            7300            7310            7320
ATTAGTTCAT  AGCCCATATA  TGGAGTTCCG  CGTTACATAA  CTTACGGTAA  ATGGCCCGCC
TAATCAAGTA  TCGGGTATAT  ACCTCAAGGC  GCAATGTATT  GAATGCCATT  TACCGGGCGG

      7330            7340            7350            7360            7370            7380
TGGCTGACCG  CCCAACGACC  CCCGCCCATT  GACGTCAATA  ATGACGTATG  TTCCCATAGT
ACCGACTGGC  GGGTTGCTGG  GGGCGGGTAA  CTGCAGTTAT  TACTGCATAC  AAGGGTATCA

      7390            7400            7410            7420            7430            7440
AACGCCAATA  GGGACTTTCC  ATTGACGTCA  ATGGGTGGAC  TATTTACGGT  AAACTGCCCA
TTGCGGTTAT  CCCTGAAAGG  TAACTGCCAGT  TACCCACCTG  ATAAATGCCA  TTTGACGGGT

      7450            7460            7470            7480            7490            7500
CTTGGCAGTA  CATCAAGTGT  ATCATATGCC  AAGTACGCCC  CCTATTGACG  TCAATGACGG
GAACCGTCAT  GTAGTTCACA  TAGTATACGG  TTCATGCGGG  GGATAACTGC  AGTTACTGCC

      7510            7520            7530            7540            7550            7560
TAAATGGCCC  GCCTGGCATT  ATGCCCAGTA  CATGACCTTA  TGGGACTTTC  CTACTTGGCA
ATTTACCGGG  CGGACCGTAA  TACGGGTCAT  GTACTGGAAT  ACCCTGAAAG  GATGAACCGT

      7570            7580            7590            7600            7610            7620
GTACATCTAC  GTATTAGTCA  TCGCTATTAC  CATGGTGATG  CGGTTTTGGC  AGTACATCAA
CATGTAGATG  CATAATCAGT  AGCGATAATG  GTACCACTAC  GCCAAAACCG  TCATGTAGTT

      7630            7640            7650            7660            7670            7680
TGGGCGTGGA  TAGCGGTTTG  ACTCACGGGG  ATTTCCAAGT  CTCCACCCCA  TTGACGTCAA
ACCCGCACCT  ATCGCCAAAC  TGAGTGCCCC  TAAAGGTTCA  GAGGTGGGGT  AACTGCAGTT

      7690            7700            7710            7720            7730            7740
TGGGAGTTTG  TTTTGGCACC  AAAATCAACG  GGACTTTCCA  AAATGTCGTA  ACAACTCCGC
ACCCTCAAAC  AAAACCGTGG  TTTTAGTTGC  CCTGAAAGGT  TTTACAGCAT  TGTTGAGGCG

      7750            7760            7770            7780            7790            7800
CCCATTGACG  CAAATGGGCG  GTAGGCGTGT  ACGGTGGGAG  GTCTATATAA  GCAGAGCTCT
GGGTAACTGC  CTTTACCCGC  CATCCGCACA  TGCCACCCTC  CAGATATATT  CGTCTCGAGA
```

FIGURE 19N

(SEQ ID NO. 23)

pD17-hG1b

```
        7810        7820        7830        7840        7850        7860
CTGGCTAACT AGAGAACCCA CTGCTTACTG GCTTATCGAA ATTAATACGA CTCACTATAG
GACCGATTGA TCTCTTGGGT GACGAATGAC CGAATAGCTT TAATTATGCT GAGTGATATC

        7870        7880
GGAGACCCAA GCTT
CCTCTGGGTT CGAA
```

Figure 26

hBR96-2 Heavy Chain Variable Region (V$_H$)

```
1              11             21            31             41
EVQLVESGGG  LVQPGGSLRL  SCAASGFPFS  DYYMYWVRQA  PGKGLEWVSY
51         61             71            81             91
ISQDGDITDY  ADSVKGRFTI  SRDNAKNSLY  LQMNSLRDED  TAVYYCARGL
101           111
ADGAWFAYWG  QGTLVTVSS  (SEQ ID NO. 24)
```

human IgG1 constant

```
          |CH1
          A STKGPSVFPL  APSSKSTSGG  TAALGCLVKD
YFPEPVTVSW  NSGALTSGVH  TFPAVLQSSG  LYSLSSVVTV  PSSSLGTQTY
ICNVNHKPSN  TKVDKKVEPK  SCDKTHTCPP  C|CH2
                                     APEICGP  SVFLFPPKPK
DTLMISRTPE  VTCVVVDVSH  EDPEVKFNWY  VDGVEVHNAK  TKPREEQYNS
                          318 320 322              334
TYRVVSVLTV  LHQDWLNGKE  YKCKVSNKAL  PAPIEKTISK  AKGQPREPQV
                                                  |CH3
YTLPPSRDEL  TKNQVSLTCL  VKGFYPSDIA  VEWESNGQPE  NNYKTTPPVL
DSDGSFFLYS  KLTVDKSRWQ  QGNVFSCSVM  HEALHNHYTQ  KSLSLSPGK
```

(SEQ ID NO. 25)

Figure 27

hBR96-2A: Heavy Chain Variable Region (V_H)

```
1          11         21         31         41
EVQLVESGGG LVQPGGSLRL SCAASGFPFS DYYMYWVRQA PGKGLEWVSY

51         61         71         81         91
ISQDGDITDY ADSVKGRFTI SRDNAKNSLY LQMNSLRDED TAVYYCARGL

101        111
ADGAWFAYWG QGTLVTVSS (SEQ ID NO. 24)
```

hBR96-2A: Human Heavy Chain IgG1 Constant Region ΔCH2

```
A STKGPSVFPL APSSKSTSGG TAALGCLVKD YFPEPVTVSW NSGALTSGVH

TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY ICNVNHKPSN TKVDKKVEPK

SCDKTHTCPP CP    GQPREPQV YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA

VEWESNGQPE NNYKTTPPVL DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM

HEALHNHYTQ KSLSLSPGK (SEQ ID NO. 26)
```

Figure 28

This sequence is the chi BR96 IgG1 with CH2 deleted.

VH

```
  1  EVNLVESGGG LVQPGGSLKV SCVTSGFTFS DYYMYWVRQT PEKRLEWVAY

 51  ISQGGDITDY PDTVKGRFTI SRDNAKNTLY LQMSRLKSED TAMYYCARGL
                          CH1
101  DDGAWFAYWG QGTLVTVSVA STKGPSVFPL APSSKSTSGG TAALGCLVKD

151  YPPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY
                                        CH3
201  ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CHGQPREPQV YTLPPSRDEL

251  TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS

301  KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK
```

(SEQ ID NO. 27)